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# Virtual population analysis

## A practical manual for stock assessment

FAO FISHERIES TECHNICAL PAPER

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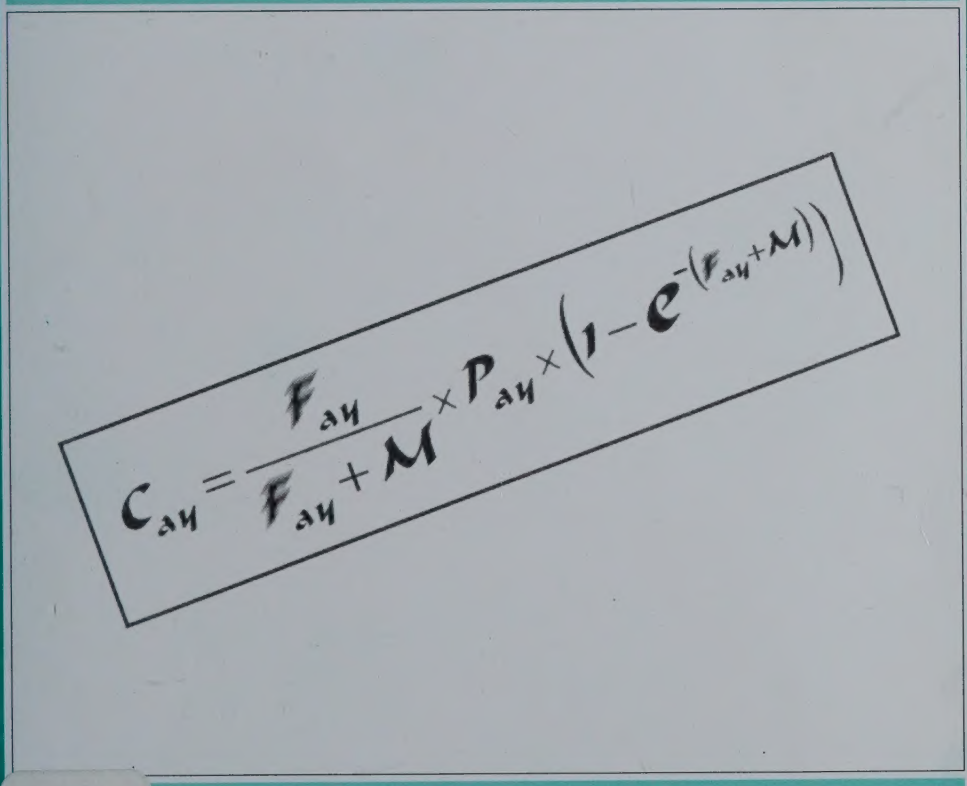


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## A practical manual for stock assessment

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Rome, 2001

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## PREPARATION OF THIS DOCUMENT

The FAO/DANIDA project GCP/INT/575/DEN "Training in Fish Stock Assessment and Fishery Research Planning" organized some 100 Training Courses and Workshops dealing with fish stock assessment from 1983 to 1998. This document is based on lecture material that was gradually developed for three high-level regional courses given in 1996 at IMARPE, in Callao, Peru for Latin America, in cooperation with the Comisión Permanente del Pacífico Sur (CPPS), in 1997 in Hillerød, Denmark for countries bordering the Baltic Sea in cooperation with the International Council for the Exploration of the Sea (ICES) and in 1998 at NATMIRC in Swakopmund, Namibia for Angola, Namibia and South Africa, in cooperation with the Nansen Programme. The material was further tested in a course held in Valparaiso, Chile in December 1999, organized under a bilateral agreement between Chile and Denmark.

The following scientists have contributed to the contents of this manual and the accompanying exercises: Ana-Maria Caramelo (FAO), Pavel Gassioukov (Russia), Renato Guevara (Peru), Eskild Kirkegaard (Denmark), Hans Lassen (ICES), Jean-Jacques Maguire (Canada), Paul Medley (UK), Christian Riise (FAO), Henrik Sparholt (ICES), Bernard Vaske (Namibia), Siebren Venema (FAO) and Alejandro Zuleta (Chile).

The lecture material underwent gradual modifications and finally a draft manual was produced by Hans Lassen in 1998. This draft was subsequently revised and expanded by Paul Medley, in close cooperation with Hans Lassen. For this work some funds were used of the FAO/Norway FISHCODE project GCP/INT/648/NOR.

ICES kindly gave permission to use selected data sets for the exercises. Use has been made of software provided by Numerical Recipes Software, Cambridge MA, USA, for which permission was requested

The document covers most of the stock assessment methods that are presently in use in countries and areas where sophisticated data collection systems provide the necessary data. It is the last, and most advanced manual in a series on fish stock assessment and data collection, developed between 1983 and 1998 by the FAO/DANIDA project GCP/INT/575/DEN.

In addition to the printed document, a compact disk is provided that contains a series of exercises and examples that should facilitate the application of these methods in countries where good data are being made available.

Siebren C. Venema
Project Manager

Lassen, H.; Medley, P.
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(Includes a CD Rom containing additional examples and exercises.)

**ABSTRACT**

Virtual Population Analysis (VPA) is a widely used model for the analysis of fished populations. While there are very many VPA techniques, they vary in the way they use data and fit the model rather than in the form of the model itself. This manual describes the common VPA model and the assumptions on which it is based, together with descriptions of associated diagnostic procedures and common reference points. More importantly, the manual describes the numerical techniques which can be used to fit the model based on weighted least-squares, which is the basis for the ADAPT approach. The techniques are described so that they are readily implemented in a spreadsheet. General methods and specific examples are given to enable the readers to develop an approach suitable for their own data and fisheries.

**Distribution:**

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# GLOSSARY AND ACRONYMS

| Term | Full Name | Description | Reference |
|---|---|---|---|
| **ADAPT** | Adaptive framework | A general approach to fitting VPA models. ADAPT is based on minimising the sum-of-squares over any number of indices of abundance to find best-fit parameters. | Gavaris (1988) |
| **ALK** | Age-length key | A table relating ages and lengths of a fish species | |
| **CAGEAN** | Catch-at-AGE Analysis | Equivalent to ADAPT with separable VPA, but with more emphasis on the statistical rather than biological model. | Deriso *et al.* (1985) |
| **CCAMLR** | Commission for the Conservation of Antarctic Marine Living resources | | |
| **CECAF** | Fishery Committee for the Eastern Central Atlantic | | |
| **CPUE** | Catch per Unit of Effort | | |
| **ICA** | Integrated Catch-at-age Analysis | Equivalent to ADAPT, i.e. using a least-squares fit based on VPA and auxillary data, but the standard VPA catch formulation used in ADAPT is replaced by a separable VPA. | Patterson and Melvin (1995) |
| **ICES** | International Council for the Exploration of the Sea, based in Copenhagen | | |
| **Multispecies VPA** | Multispecies Virtual Population Analysis | Extends the cohort model with a model for the natural mortality that includes predator-prey relationships. Data as for VPA for all stocks, as well as stomach contents from at least one sample survey. | Sparre (1992)<br><br>Magnusson (1995) |
| **Pope's Cohort Analysis** | | As with VPA, but the non-linear catch equation is replaced with an approximate explicit solution. | Pope (1972) |
| **Separable VPA** | Separable Virtual Population Analysis | The fishing mortality in the normal VPA model is separated into an exploitation rate and selectivity, which multiplied together estimate the fishing mortality. This produces estimates of catches, which can be fitted to observed catches even if no indices are available. | Pope and Shepherd (1982) |
| **SPA** | Sequential Population Analysis | Equivalent to VPA. This is the more common term used in USA and Canada. | |
| **Survivor Analysis** | | Analysis where the survivors are the focus of estimation rather than fishing mortality. Equivalent to VPA. | Doubleday (1976) |
| **TAC** | Total Allowable Catch | Management measure. The total amount of catch allowed to be taken from a particular stock in a particular year. | |

| | | | |
|---|---|---|---|
| **VPA** | Virtual Population Analysis | A general method to model the progression of a cohort through time. VPA became useful when the Baranov catch equation incorporating observed catches could be solved sequentially. | Gulland (1965)<br><br>Fry (1949) |
| **XSA** | Extended Survivor Analysis | A VPA with no catch errors is tuned with age-specific CPUE indices. The model is fitted through a specialised robust iteration technique, rather than general least-squares. The procedure includes an iterative weighting of CPUE indices. | Shepherd (1991, 1999) |

# 1 INTRODUCTION

## 1.1 OVERVIEW

There are a variety of VPA-type methods, which form powerful tools for stock assessment. At first sight, the large number of methods and their arcane names can put off the newcomer. However, this complexity is based on simple common components. All these methods use age-structured data to assess the state of a stock. The stock assessment is based on a population dynamics model, which defines how the age-structure changes through time. This model is the simplest possible description of numbers of similar aged fish where we wish to account for decreases in stock size through fishing activities. The diversity of VPA methods comes from the way they use different types of data and the way they are fitted.

This manual is structured to describe the different components that make up a VPA stock assessment model:

**Population Model** (Analytical Model) The population model is the common element among all VPA methods. The model defines the number of fish in a cohort based on the fishing history and age of the fish. A cohort is a set of fish all having (approximately) the same age, which gain no new members after recruitment, but decline through mortality. The fisheries model attempts to measure the impact catches have on the population. The population model usually will encapsulate the time series aspects of change and should include any random effects on the population (process errors), if any.

**Link Model** Only rarely can variables in which we are interested be observed directly. Usually data consists of observations that are only indirectly linked to variables of interest in the population model. The models linking the population model to observable variables are many and varied. They, in general, separate the different VPA approaches. The most common observable variable is CPUE (Catch per Unit of Effort), which is often thought to be related to stock size. The link model in most cases will be associated with an observation error.

**Error Model** Finally, the model needs to be fitted to observations. The error model defines the criteria to do this, so that some objective best-estimate for the parameters and stock status are obtained. In VPA, weighted least-squares is often used as the fitting procedure, and this is the method discussed in this manual. A broadening of this approach allows the population and link models to describe parameters in any likelihood function. Although this latter approach may be preferred, it is more complicated and not discussed in detail in the manual.

The reason for discussing the models as separate components is because there is no general prescriptive VPA method. Instead, the readers should be able to use the components to develop VPAs suitable for their own fisheries. This manual aims to provide the readers with a degree of understanding so that they will be able to use

spreadsheets and other software tools to carry out the numerical procedures necessary to conduct a non-standard VPA.

The methods explained are for illustration only and should not be taken as an endorsement of any method in any particular case. In some of the examples, data presented were extracted from ICES assessment working group reports. These data do not represent all information available for stock assessment, as they were selected to illustrate the methods only. The results differ from the ICES stock assessment results and should not be used for anything other than illustrating calculations. It is hoped that the readers will be given enough insight to evaluate methods for themselves and see whether any technique is applicable to their own data and fishery.

## 1.2 BACKGROUND

Virtual or Sequential Population Analysis (VPA or SPA) was introduced in fish stock assessment by Gulland (1965) based on older work (e.g. Fry 1949). The classical VPA analysis is not a statistical analysis, however, it is an important basis for the ADAPT and other statistical methods presented in the manual. The method is also very useful in itself as a tool for exploratory data analysis. For heavily exploited fish stocks, the method provides a good estimate of the recruitment of cohorts that have passed through the fisheries. Similarly, the estimate of fishing mortality for years dominated by cohorts that have passed through is fairly reliable provided the exploitation rate is high compared to the natural mortality. For a general discussion of the behaviour of the VPA technique, see Megrey (1989) and Mesnil (1989).

The population or analytical model applies to the unit stock (Cushing 1981). The unit stock is a group of fish of the same species that forms a reproductive unit (e.g. shares spawning grounds). A unit stock is assumed to have the same life cycle, similar growth rates and in general to be a single biological unit. It is assumed that there is no emigration or immigration (closed populations). However, some types of emigration can be incorporated in the model by assuming it as part of the age-dependent natural mortality. Explicitly including immigration and emigration requires that both the stock losing fish and the stock receiving fish be assessed simultaneously.

The unit stock is broken down into cohorts. A cohort is a group of fish that have the same age. This means that a cohort will have more or less the same size and will often be found in the same area at any point in time. Furthermore, a cohort will mature at the same time. The use of the cohort model requires an empirical method to separate different cohorts, usually through ageing based on otoliths or scales (Holden and Raitt 1974).

The population model is most often used in a single-species version. It is usually assumed that species interactions do not introduce variation in mortality or growth rates between years (i.e. $M$ is constant from year to year). This assumption is relaxed in multispecies VPA (briefly described in Section 4.8).

VPA methods have been grouped in a number of ways:

- Based on the restrictions imposed in the data model; for example, Extended Survivor Analysis (XSA) does not include biomass indices for tuning the VPA.

- Based on the assumptions imposed, particularly on fishing mortality; for example, the ICA and CAGEAN methods assume that the fishing mortality can be decomposed (separated) into an age and a year effect.

- Based on how the calculations are organised. For example, the Virtual Population Analysis (VPA) solves the Baranov equation directly by numerical methods, whereas Cohort Analysis, based on the same data model as VPA, uses an approximate solution to this equation. ADAPT, based on VPA, uses the fishing mortality of the terminal year and of the oldest age as the unknown parameters, whereas the XSA method uses the number of survivors of the each age group as the unknowns.

These differences revolve around the way the models are fitted and solved. In terms of results, they are of little principal importance, but often reflect the available data.

The VPA method in fish stock assessment is widely used. For example, it is used in assessing most fish stocks in the Northeast and Northwest Atlantic, and many other stocks in the Northern Pacific, Australia, New Zealand, South Africa, Argentina, Chile, Peru, in CCAMLR and CECAF. The classical presentations of this model and its applications are Beverton and Holt (1957) and Ricker (1975), who describe the single species version in detail and Jones (1984). Modern presentations are given in many textbooks (e.g. Gallucci *et al.* 1996, Hilborn and Walters 1992, King 1995, Sparre and Venema 1998). The VPA analytical model has been expanded to include multispecies interactions (Magnusson 1995, Sparre 1991). The estimation procedures used in assessment work when using the analytical model for fish stock assessment have been developed in the 1980s and early 1990s (see Conser 1993, for a historic review of ADAPT). These new methods include least-squares estimation of the state of the stock using both catch/effort and survey data in an integrated fashion. In more recent years, Bayesian methods have been introduced to fish stock assessment for estimation of parameters and their variances by calculating the full parameter joint probability distributions (Walters and Punt 1994, Punt and Hilborn 1997, and Virtala *et al.* 1998 for an application to VPA). Bayesian methods are more complicated than the procedures presented in this manual. However, the methods used here would, in almost all cases, be a recommended preliminary analysis in a Bayesian assessment.

VPA is not the only approach to fish stock assessment. Alternative approaches include dynamic biomass models, (e.g. Punt and Hilborn 1996), length-based methods, (e.g. Sparre and Venema 1998, King 1995), heuristic analysis of trends in catch and CPUE data (King 1995, Gallucci *et al.* 1996) and production approaches such as the ECOPATH model (Christensen and Pauly 1992).

# 2 OBJECTIVES

The purpose of fish stock assessment is to provide estimates of the state of the stock. The state of a stock is defined by its abundance at a specific time, together with the mortality and growth that control its development. The use of these estimates varies, from ecological studies, where the fish stock is only one of several components of the ecosystem, to fisheries management advice where the stock abundance forms the basis for reviewing different fishing options. Because of this latter application, fish stock assessment pays particular attention to the influence of fishing on stock development. In this case, total mortality is split into changes caused by fishing and changes caused by "other" factors. This "other" component can then be broken down into contributions from predation, disease etc.

The fish stock assessment procedure is built of three parts:

- An estimate of the current stock status,
- A projection of the yield, total and spawning stock biomass and recruitment for specified scenarios of fishing mortalities, and
- The relationship between the stock status / projection and a number of biological reference points.

These parts are used to formulate biological advice on fishery management, and evaluate whether the stock is within safe biological limits, i.e. productivity (growth, recruitment) is not adversely affected by fishing.

The stock status is defined by the:

- Stock size, the number of fish by age group at a particular point in time,
- Stock productivity, growth, maturity, fecundity and recruitment, and
- Stock mortality, made up of fishing and natural mortality rates.

This manual focuses on the estimation of the number of fish and the mortality by age group for a series of years. This procedure also provides an estimate of recruitment. The other information necessary for a full assessment, growth, maturity and fecundity, are estimated by other methods than those included in this manual and are not discussed (see Holden and Raitt 1974). However, this information is often needed as input to methods discussed in this manual (e.g. for estimation of yield-per-recruit reference points).

Stock assessment results are usually given as estimates of the state variables of the stock (numbers-at-age) and projections based on estimates of stock dynamics parameters:

- Abundance of older age groups

- Recruitment
- Mortalities exerted on the population by both fishing and natural causes
- Spawning stock biomass
- Growth parameters
- Relating the stock development to a number of biological reference points based on fishing mortality, spawning stock biomass and recruitment.
- Providing projections of yield, spawning stock biomass and recruitment for specified scenarios of fishing mortality over the short (about 2 years), medium (5-10 years) and long (equilibrium) terms.
- Providing an evaluation of the status of the stock within safe biological limits (i.e. productivity not adversely affected by fishing) and outside safe biological limits (i.e. growth and/or recruitment adversely affected by fishing).

# 3 WHEN TO USE VPA

VPA methods require age-structured data, and, in general, VPA-type methods are always preferable when age-structured data are available. Catch-at-age data are usually derived from large scale size frequency sampling, and smaller scale age sampling to provide age-length keys (ALK). Age-length keys also can be obtained, but less reliably, from growth models, but in either case size and age need to be linked through models. Alternatively, the age distribution can be obtained directly by sampling the catches and ageing the entire sample, although often it is difficult to get good coverage at low cost using this approach.

The catch in number of fish and mean weights are usually derived from total yield (catch in weight) data from a fisheries statistics programme and biological samples taken from these catches. The biological data provide the mean weight of individuals, which can be used to convert weight to numbers. The age composition of the catch can be obtained from age-length keys or aged random samples of the catches.

The VPA model was built on the assumption that there is one cohort per year. This is not a serious restriction, but the model needs modifications when there are several cohorts per year. The usual difficulty in dealing with more than one cohort per year is the lack of methods to allocate fish to their correct cohort. There are examples when there is no cohort structure in the population because the fish stock is spawning continuously. The population model applicable in such a situation differs from that presented in this manual.

The general data model includes the following elements, but only rarely are all elements available for a particular assessment.

- Total catch in number by age and year.
- Abundance estimates in absolute terms, each index representing one or several age groups (e.g. acoustic survey abundance estimates).
- Abundance indices, each index representing one or several age groups (e.g. bottom trawl CPUE from research vessel surveys).
- Biomass indices, typically representing several age groups (e.g. spawning stock biomass indices from egg or larvae surveys).
- Effort indices, typically representing the partial fishing mortality on a group of age classes (e.g. effort data from a fisheries statistics logbook programme).
- Mean weights by age and by year corresponding to the catch. These data are not used in the stock estimation procedure that is directed towards obtaining stock in numbers by age and by year. The mean weights are, however, used in projections of the yield under different scenarios.

The following three data types are required for calculation of the spawning stock biomass:

- Mean weights by age and by year corresponding to the spawning stock
- Maturity ogive (fraction of the population which are mature) by age and by year
- Fractions of the mortality prior to spawning

The total catch data take a special role in this model. While some of all the other elements may be missing, this is not the case with the catch-at-age and year data. These data must be available for the methods presented in this manual to be applicable. In Section 7.4 methods dealing with missing values in the catch-at-age and year data matrix are considered.

Natural mortality is only rarely estimated using VPA. Vetter (1988) reviewed methods to obtain the natural mortality. The parameter can in some cases be estimated from the types of data discussed in this manual. However, experience has shown that where such estimates can be obtained, they have very large confidence limits and are therefore not considered useful.

Useful information on natural mortality can be obtained through the Multispecies VPA technique (Sparre 1991, Magnusson 1995, Section 4.8). Here the standard data model is extended with data on stomach contents from fish caught at sea and with data from laboratory experiments, providing estimates of annual prey consumption.

# 4 THE POPULATION MODEL

The state of the stock at a specific point in time is described by:

- Stock in numbers by age group (cohort)
- Mean weight per individual in the stock by age group
- Mean weight per individual in the catch by age (sometimes these weights are specified for a number of fleets)
- Maturity proportion by age group

The stock development is based on a number of processes:

- **Growth.** The classical description of growth is the von Bertalanffy model, but it is often described without a model, simply as an age group vector of mean weight per individual.
- **Recruitment.** This is often described as a function of the spawning stock biomass only: $R = R(SSB)$ or as a simple white noise random process.
- **Survival.** $N_{age+\Delta t} = N_{age}\, e^{-Z\,\Delta t}$. The total mortality $Z$ is decomposed into fishing mortality ($F$) and natural mortality ($M$): $Z = F + M$
- **Fishing mortality.** ($F$) is a process independent of natural mortality ($M$). Fishing mortality is usually estimated for each year and age group combination separately, i.e. fishing mortality and the exploitation pattern vary between years.
- **Natural mortality.** ($M$) is described either as an age dependent fixed parameter $M = M(age)$ or as a multispecies interactive process: $M = M(age, other\ populations)$. Natural mortality can implicitly account for emigration. As natural mortality is often assumed at least to be a stationary process (i.e. independent of time) then emigration is assumed to have similar characteristics. The emigration rate therefore is usually assumed to depend on age only, without year-to-year variation.

## 4.1 THE COHORT MODEL

The analytical model follows a cohort from year to year. A cohort is subject to total mortality ($Z$), which defines the rate of decrease of the population size ($P$). In the fisheries version of the cohort model, this mortality is decomposed into a fisheries contribution ($F$), and contribution from all other sources, the natural mortality ($M$). These processes are assumed to operate without interference.

$$Z = F + M \tag{1}$$

$$\frac{dP}{dt} = -ZP = -(F+M)P \qquad (2)$$

The interpretation of these mortalities is as instantaneous mortality rates and within a time interval where these rates are constant, we get an exponential decrease in numbers:

$$P_{a+1,y+1} = P_{ay}\, e^{-Z_{ay}} \qquad (3)$$

or, in logarithmic form:

$$\ln P_{a+1,y+1} = \ln P_{ay} - Z_{ay} \qquad (4)$$

The logarithmic form will be used in the cohort model.

Often the final age group accumulates survivors. The minimum age for this group is often chosen either because it is not possible to distinguish individuals by size at this age as they have reached their growth limit or the numbers in this group is very small relative to others in the catch. This "plus" group consists of members surviving from the previous year as well as adding additional cohorts as they reach the group's minimum age:

$$P_{A,y+1} = P_{Ay}\, e^{-Z_{Ay}} + P_{A-1,y}\, e^{-Z_{A-1,y}} \qquad (5)$$

where $P_{Ay}$ = the population size in the plus group with minimum age $A$.

## 4.2 THE CATCH MODEL

The decomposition of the total mortality into natural and fishing mortality is required because we only observe the catch, $C$, and not the other deaths. The solution is derived using a similar argument as above:

$$\frac{dC}{dt} = F\,P \qquad (6)$$

which, when $F$ is constant, has the solution:

$$C_{ay} = P_{ay}\, F_{ay}\, \frac{1-e^{-Z_{ay}}}{Z_{ay}} \qquad (7)$$

or, in logarithmic terms:

$$\ln C_{ay} = \ln P_{ay} + \ln F_{ay} + \ln\left(\frac{1-e^{-Z_{ay}}}{Z_{ay}}\right)$$

with (8)

$$Z_{ay} = F_{ay} + M_a$$

where $P_{ay}$ is the population size at the beginning of the time period $y$, $C_{ay}$ is the catch during the period, and $F_{ay}$ and $M_a$ are assumed to be constant during the period. Equation 7, sometimes known as the Baranov catch equation, cannot be solved for $P_{ay}$ or $F_{ay}$ directly, as it is transcendental. It can only be solved through numerical techniques such as Newton-Raphson Iteration (Section 4.7.1) and Functional Iteration (Section 4.7.2). However, any method for solving non-linear equations can serve.

Equation 7 is, in essence, a deterministic time series population model. This can be seen more clearly by rewriting it in terms of the population sizes rather than fishing mortality:

$$Z_{ay} = \ln P_{ay} - \ln P_{a+1,y+1}$$

$$\mathrm{F_{ay}} = Z_{ay} - M_a \quad (9)$$

$$\therefore \quad C_{ay} = \left[1 - \frac{M_a}{\ln P_{ay} - \ln P_{a+1,y+1}}\right]\left(P_{ay} - P_{a+1,y+1}\right)$$

Given values for $C_{ay}$, $M_a$ and either one of the two population sizes, $P_{ay}$ or $P_{a+1,y+1}$, or $F_{ay}$, the remaining variables can be calculated. In other words, there is only one exact solution. This contrasts with a statistical model where there is no exact solution, but we identify one that is the 'best fit'.

As has been noted, the same model can be rewritten in a number of different algebraic forms. This is done for mathematical convenience, but makes no difference to the results. For example, we can either have the initial population, $P_{ay}$, and calculate forwards or the final population, $P_{a+1,y+1}$ , and calculate backwards. In either case, there is only one identical solution.

## 4.3 COHORT PROJECTIONS

By solving a series of Equation 7, the sequence of $F$'s and $P$'s for each cohort can be defined. However, to start this process, at least one $F$ or $P$ is needed for each cohort. This is usually the terminal $F$. Given the terminal $F$, the cohort size at the beginning of the last period can be calculated as:

$$P_{ay} = \frac{C_{ay}\, Z_{ay}}{\left(1-e^{-Z_{ay}}\right)F_{ay}} \quad (10)$$

where the subscript $ay$ refers to the last age or year, as appropriate. In classical VPA these parameters are pre-defined, but in tuned VPA, they are estimated from other data.

In the model, each cohort is separate and therefore can be calculated independently. In practice, data often extend across cohorts, so this independence is lost when fitting the model to real data. The cohorts are therefore usually jointly represented in a matrix form, with years forming the columns and ages forming the rows (**Figure 4.1**).

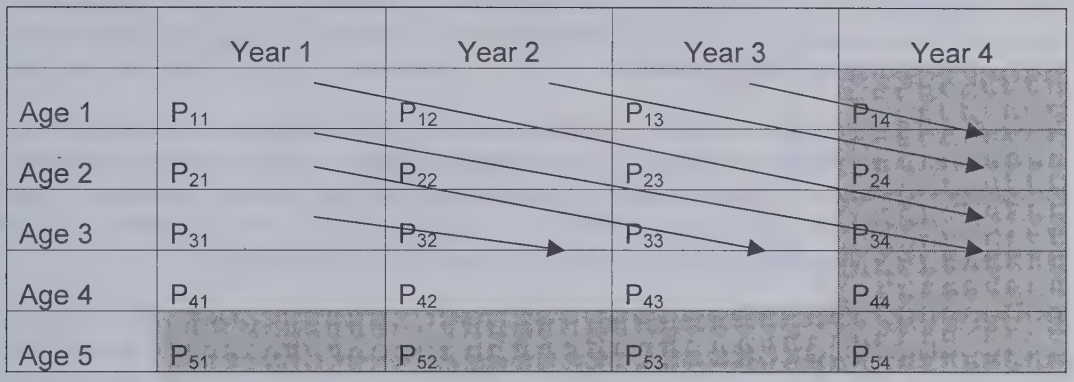


**Figure 4.1 The age-year matrix illustrating cohorts. The arrows, moving diagonally through the matrix, indicate the relationships defined by Equation 7. Shaded cells are the terminal age group / year which require a parameter each to complete the cohort calculations.**

As in the case of the single cohort, the population equations do not fully determine the entire matrices $\{P\}_{ay}$. There is a set of $A+Y-1$ $F$'s (or $P$'s) that together with the natural mortality $M_a$ cannot be estimated as there are an infinite number of solutions that fulfil the criteria set up by the equations. In classical VPA, these are provided as external parameters.

The external parameters required for the solution of these equations include the fishing mortality for the terminal year and the fishing mortality for the oldest age group for all years. An equivalent set of external parameters that are used in some formulations is the number of survivors of the terminal year and of the terminal age group. This is sometimes more convenient in arranging the calculations. It also has the advantage that it is the number of survivors of the terminal year that is essential to the projections on which the biological advice is based. It is therefore useful that the variance of survivor estimates is derived directly in the estimation procedure.

## 4.4 SEPARABLE VPA

Under normal VPA the fishing mortality for each age in each year is calculated, still leaving us short of the terminal $F$'s, which must be provided. In essence, the $F_{ay}$ are parameters which equal the number of catch-at-age data. Given the end (or start) population sizes, the full model has one solution. Introducing an additional model describing the relationship between fishing mortalities effectively can reduce this

number of parameters. The separable model separates the exploitation rate from the selectivity pattern. The assumption is that the exploitation pattern remains constant over some significant period of time and only the overall level of exploitation varies between years, so that:

$$F_{ay} = S_a E_y \tag{11}$$

The fishing mortality is separated into an age-dependent exploitation pattern ($S_a$) and an age-independent exploitation level ($E_y$), which may be parameters or a fishing effort data series. Now instead of estimating the individual $F_{ay}$'s, we use the catch data to estimate the $S_a$ and $E_y$. This can be done by substituting $S_a E_y$ in Equation 11 for $F_{ay}$ in the population model (Equation 7) and the terminal $F$ equation defining the final population size (Equation 10).

As well as reducing the number of parameters, the separable VPA model has the advantage in projecting the effects of future fishing activities. For example, very often the selectivity pattern is gear-dependent and it changes only slowly compared to the level of exploitation. This allows projections to based upon the variation of one parameter over time which is much easier to understand and carry out.

The separable VPA model has advantages only for longer time series with several age classes. With every one year's data that are added, we only add one parameter to the model, but a number of data points equaling the number of age classes. In other words, the number of data points increases relative to the number of parameters leading to a more reliable fit. When this model has fewer parameters than data, there is no exact solution and it is necessary to fit the model using principles such as least-squares (Section 4.7.3).

Pope and Shepherd (1982) proposed the formal analysis as separable VPA. They discuss the simple situation when there is only catch-at-age in numbers available. This method was extended by Deriso *et al.* (1985) and Patterson and Melvin (1995) to include tuning data (i.e. abundance indices from research vessel surveys or commercial CPUE data).

## 4.5 POPE'S APPROXIMATION

Pope (1972) proposed a very simple approximate solution to the Baranov equation:

$$N_a = N_{a+1} e^{M_a} + C_a e^{M_a/2}$$

and (12)

$$F_a = \ln\left(\frac{N_a}{N_{a+1}}\right) - M_a$$

This is, essentially, a linear approximation to the transcendental Equation 7. It depends mathematically on the approximation:

$$e^{M/2} \approx \frac{Z(1-e^{-F})}{F(1-e^{-F})} \qquad (13)$$

In modelling terms, it assumes that all fishing takes place instantaneously in the middle of the year. This removes the effect of a declining catch rate within the year as the cohort declines. In cases of low fishing mortality, it is often a good approximation (Figure 4.2).

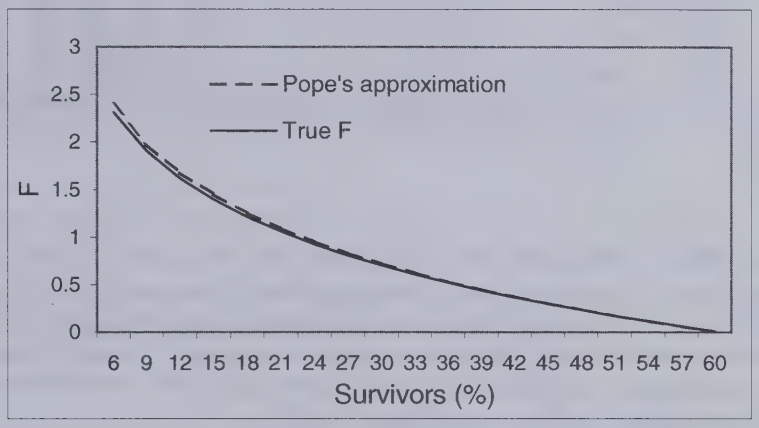


**Figure 4.2 A comparison between Pope's cohort approximation and the exact solution to the Baranov equation (M = 0.5).**

Although Pope's model is usually thought of as an approximation to the solution to the Baranov equation, it may actually also be considered as a model in its own right. The Baranov equation assumes that fishing with constant fishing mortality is spread throughout the time period considered, e.g. a year. Pope's cohort model describes "pulse fishing", where the fishing takes place in a single moment in the middle of the year. Based on that model the constant, ½, would be replaced with some other value if the pulse fishing takes place at a different time of the year. For example, if fishing occurred on the 1st April, the constant would be ¼. In both these models, the natural mortality $M$ is assumed constant over the year, perhaps unlikely because of the annual cycle in the biological productivity. For a further discussion of the interpretation of these models, see MacCall (1986).

## 4.6 CONVERGENCE BEHAVIOUR OF THE VPA PROCEDURE

The VPA procedure is simply using the summed catches weighted by the natural mortality as the stock estimate. This can be seen more clearly from Pope's cohort model. This suggests that when fishing mortality is high the recruitment estimate is insensitive to the initial guess on survivors or fishing mortality of the oldest age group. This is because remaining fish that are assumed to be still alive will be only a small fraction of the total recruitment. The number of fish actually observed in the catches will dominate the total recruitment. This is the "convergence behaviour" of VPA (Figure 4.3).

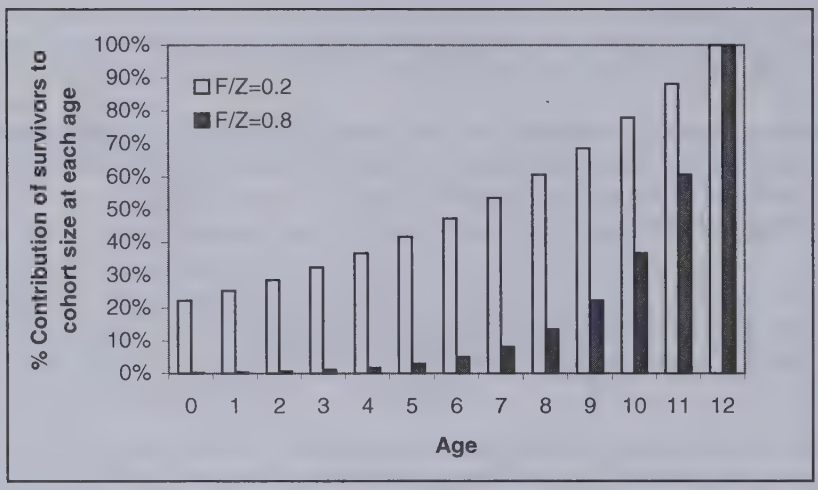


**Figure 4.3 Age 12 fish as the proportion of the cohort size at each age, illustrating the influence of terminal survivors on the VPA stock estimate. Where F/Z=0.2, the percentage of the cohort dependent on the survivors remains high, making up 22% of the original recruits. Where F is much higher, survivors contribute very little to recruitment estimate, which now statistically depends much more on the sum of past catches.**

If the fishing mortality is low then survey results and other "tuning" data will have a major impact on the fitted historical pattern of stock sizes and fishing mortalities, while if fishing mortality is high (compared to the natural mortality) then this influence is much less. The terminal year is of special interest for fisheries management applications. The estimate of the state of the stock in this year is the starting point for projections that form the basis for calculation of TAC's and other possible regulatory measures that are required to meet the management objectives. So, while the historical pattern may be well estimated in a situation with high fishing mortality, this may not be the case for state of the stock in the terminal year. We shall return to this problem later.

## 4.7 SOLVING THE VPA EQUATIONS

### 4.7.1 Newton-Raphson Iteration

The Newton-Raphson method works efficiently and the procedure can be extracted from any computer program library on numerical methods (e.g. Press *et al.* 1989). The first derivative can be found directly or, as with most modern numerical methods, through a numerical approximation to the derivative.

The simplest method uses the population Equation 9, rearranged into a form where the evaluation as a function of $N_a$ is zero.

$$f(N_a)=\left[1-\frac{M}{Z}\right](N_a - N_{a+1})$$

where (14)

$$Z = \ln(N_a)-\ln(N_{a+1})$$

and its derivative with respect to $N_a$ is:

$$f'(N_a)=1-\left(Z-\frac{(N_a - N_{a+1})}{N_a}\right)\frac{M}{Z^2} \quad (15)$$

These functions are equivalent to Equation 7, but in a form to solve for $N_a$. To obtain the value of $F$ requires the additional calculation once all $N_a$'s for the cohort have been obtained:

$$F = \ln(N_a)-\ln(N_{a+1})-M \quad (16)$$

The initial value for the iteration can easily be obtained from Pope's approximation, which leads to rapid discovery of the solution (Macro 4.1).

**Macro 4.1 The following procedure, written in Visual Basic, but easily translated into other languages, uses Equations 14 and 15 to solve the Baranov equation. It has three parameters, natural mortality, the catch and cohort size one age unit later.**

```
Function SolBaranov(M as Double, Ca as Double, Na_1 As Double) As Double
Dim fx as Double, dfx as Double, Na as Double, DeltaNa as Double, Z As Double
Na = Na_1 * Exp(M)                          'Calculate Na with no fishing
DeltaNa = Ca * Exp(M / 2)                   'Calculate Pope's fishing mortality
                                            approximation
Do While Abs(DeltaNa) > 0.1                 'Test current accuracy
Na = Na + DeltaNa                           'Add correction to Na
Z = Log(Na) - Log(Na_1)                     'Calculate total mortality
fx = (1 - M / Z) * (Na - Na_1) – Ca         'Calculate the function
dfx = 1 - (Z - (Na - Na_1) / Na) * M / (Z * Z)   'And its derivative
DeltaNa = -fx / dfx                         'Calculate the new correction factor
Loop
SolBaranov = Na                             'Return solution
End Function
```

The equation can be solved for $F$ rather than $N_a$ in much the same way. However, the iteration may in some cases run wild and give negative results. It is therefore advised that instead of solving the Baranov equation directly for the fishing mortality it is rather the logarithm of the fishing mortality that should be found. Hence,

$$f(D) = C_a - N_{a+1}\frac{e^D}{e^D + M}\left(e^{e^{D+M}} - 1\right)$$

where

$$D = \ln F \tag{17}$$

$$f'(D) = -N_{a+1}\frac{e^D}{e^D + M}\left(\frac{M}{e^D + M}\left(e^{e^{D+M}} - 1\right) + e^D e^{e^{D+M}}\right)$$

The iteration scheme then becomes:

(i) Provide an initial estimate for the log fishing mortality parameter ($ln\ F$), usually around $F = 0.5$, $ln\ F = D = -0.693$.

(ii) Calculate an estimate of the expected catch that would have been taken with this mortality:

$$c = N_{a+1}\frac{e^D}{e^D + M}\left(e^{e^{D+M}} - 1\right) \tag{18}$$

(iii) Adjust the $D$ parameter by the ratio between the function, $f(D)$ and its derivative $f'(D)$ (Equation 17):

$$D_{new} = D + \frac{C_a - c}{c\left(\frac{M}{e^D + M} + \frac{e^D e^{e^{D+M}}}{\left(e^{e^{D+M}} - 1\right)}\right)} \tag{19}$$

(iv) Check for convergence by seeing if new $D$ parameter is significantly different from the previous one. If its is go back to step (ii), else end the procedure.

Although the scheme requires an initial guess of the logarithm of the fishing mortality, the method is robust to this initial value. Even poor guesses usually converge to the correct solution. Therefore, most stock assessment software uses a fixed initial guess on the fishing mortality such as 0.5. For very large fishing mortalities (>1.5) this procedure may not converge and it would probably be better to initiate the iteration with a large value of fishing mortality, perhaps 1 to 2. Again, using Pope's cohort approximation (Section 4.5) for a starting value would avoid this problem with large $F$'s and reduce the number of iterations (see Macro 10.2 for an implementation).

### 4.7.2 Functional Iteration

Solving the Virtual Population equations is often done through "functional iteration". Functional iteration is a method that may work in specific situations when either the problem has been formulated so that functional iterations become a natural approach or where a specific functional iteration scheme has been found.

Functional iteration is the special case where it is possible to find a function so a sequence of evaluations $\beta, g(\beta), g(g(\beta)), g(g(g(\beta))), \ldots$ converge towards a desired solution. The following algorithm illustrates how functional iteration might be used to solve for fishing mortality in VPA.

(i) Provide the terminal fishing mortality and calculate the populations for each cohort for the oldest age group:

$$P_{term} = \frac{C_{term}}{(1-\exp(-Z_{term}))\left(\frac{F_{term}}{Z_{term}}\right)} \tag{20}$$

(ii) With the next oldest age group, calculate the start cohort size, using Pope's approximation:

$$P_a = P_{a+1}e^M + C_t e^{M/2} \tag{21}$$

(iii) Calculate the fishing mortality using the new population size estimate:

$$F_a = \frac{C_t(\ln P_a - \ln P_{a+1})}{P_a - P_{a+1}} \tag{22}$$

(iv) Calculate a new population size estimate based on this fishing mortality:

$$P_a = \frac{C_t}{\left(1-e^{-F_a-M}\right)\left(\frac{F_a}{F_a+M}\right)} \tag{23}$$

(v) Check for convergence (i.e. current $P_a$ or $F_a$ evaluations have not changed much from the last iteration, less than say 0.1%). If the function has not converged, go back to step (iii).

(vi) Go to step (ii) unless all ages are complete.

**Macro 4.2 The following Visual Basic procedure solves the Baranov equation using functional iteration. This function requires the same parameters as Macro 4.1, but finds the solution in a different way. Functional iteration appears slower than the Newton-Raphson procedures, but avoids the need to calculate the derivative, which may be useful in some circumstances.**

```
Function SolVPAFI(M as Double, Ca as Double, Na_1 As Double) As Double
Dim Na as Double, PrevNa as Double, F as Double, Z As Double
Na = Na_1 * Exp(M) + Ca * Exp(M / 2)          'Calculate first approximation to Na
Do
  F = Ca * (Log(Na) - Log(Na_1)) / (Na - Na_1) 'Calculate a new F
  Z = F + M                                    'Calculate new Z
  PrevNa = Na                                  'Record previous result
  Na = Ca * Z / ((1 - Exp(-Z)) * F)            'Calculate a new population size
Loop While Abs(Na - PrevNa) > 0.1              'Test current accuracy
SolVPAFI = Na                                  'Return solution
End Function
```

The procedure may, however, not always converge dependent on how close the initial guess of the population size is to the solution. The iteration can diverge to $\pm\infty$ or oscillate between two non-solution values. A procedure fully implementing this technique would need to avoid these problems.

The reason why functional iteration works with the VPA equations can be shown by considering the dynamic behaviour of the function around its solution. A convergent sequence forms for the VPA equation if it is solved for fishing mortality, such that:

$$F = \frac{C}{P\,(1-\exp(-Z))/Z} \tag{24}$$

Let $F^*$ be the solution, and let $F = F^* - \Delta F$ be the initial guess. By substitution, this becomes:

$$F_{new} = \frac{C}{P(1-\exp(-F^* + \Delta F - M))/(F^* - \Delta F + M)} \tag{25}$$

This can be approximated using Taylor expansion around the true value $F^*$.

$$F_{new} \cong \frac{C(F^*+M)(1-\dfrac{\Delta F}{F^*+M})}{P(1-\exp(-F^*-M))}(1+\frac{\exp(-F^*-M)}{1-\exp(-F^*-M)}\Delta F) \cong$$

$$F^*\left(1-\frac{\Delta F}{F^*+M}+\frac{\Delta F}{\exp(F^*+M)-1}\right) = F^* - \Delta F\frac{F^*}{F^*+M}\left(1-\frac{1}{1+\dfrac{F^*+M}{2}+....}\right) \tag{26}$$

As the factor on $\Delta F$ lies between 0 and 1, the sequence must converge to $F^*$ if $\Delta F$ is sufficiently small such that higher terms of the Taylor series can be neglected. Hence, by sequentially replacing $P$ and $F$, the function will converge.

In the case of the VPA equations, functional iteration is not necessary, so why use it? The functional iteration scheme avoids having to find the derivatives of first or second order required by the Newton-Raphson iteration. Where parameters are related through the functions, it is necessary to construct matrices of the first or second order derivatives (see Section 6.2). This can be costly in computer time, if carried out numerically and or in researchers' time if carried out analytically. Furthermore this matrix (although symmetrical) needs to be inverted, another costly numerical operation for large matrices. The functional iteration methods were therefore derived to limit the number of evaluations and inversions of the derivative matrix required for obtaining the solution.

### 4.7.3 Least-Squares

The alternative method is to fit the expected to the observed catches. Following the least-squares approach, the estimation function to be minimised is:

$$\sum_{a\in age}\sum_{y\in year}\left[\ln C_{ay}^{\text{obs}} - \ln C_{ay}^{\text{mod}}\right]^2 = \text{MIN}\{\text{model parameters}\} \qquad (27)$$

The model involved for the catch in numbers, $C_{ay}$, is the Baranov equation:

$$\ln C_{ay}^{\text{mod}} = \ln P_{ay} + \ln\left(\frac{1-e^{-Z_{ay}}}{Z_{ay}}\right) + \ln F_{ay} \qquad (28)$$

Notice now that the catch variable on the left-hand side is the model catch, not observed catch. The result is that the model has become a statistical description rather than a deterministic population model. The cohort model links the populations at different times together in the normal way (Equation 4).

The catches in the population model are the expected rather than observed catches used in the classical VPA population model. However, if only catch data are available the model remains over-specified and will fit exactly in any case. So, if the terminal $F$ parameters are fixed, the errors can all be reduced to zero, the expected and observed catches are the same and the model is exactly equivalent to a classical VPA. In practice, this method depends on how much weight is given to the catch series compared to other tuning indices (see Section 6.2).

## 4.8 MULTISPECIES VPA

Multispecies VPA (MSVPA) includes estimation of some part of the natural mortality from additional information on predator consumption. In normal VPA, natural mortality parameters are assumed to be constant from year to year, although age dependent natural mortality is sometimes included in the assessment. MSVPA relaxes this assumption and includes estimation of some part of the natural mortality as both age and year-to-year dependent. The proportion included is the predation

part of the natural mortality, which may lead to assessments that are more accurate if it is the dominating component of natural mortality. MSVPA uses the usual catch-at-age data, but supplemented with data on stomach contents and annual feeding rates for the predators. MSVPA formulates the catch equation and the predation equations in parallel and solves the resulting set of coupled equations. This set of equations becomes quite large. Where the single species approach solves separate sets of equations for each stock, the multispecies approach solves all these equations simultaneously. Sparre (1991) and Magnusson (1995) present the procedure in detail.

The basis of MSVPA is the Baranov catch equation: $C = F\ \bar{N}$, where $C$ is the catch rate in numbers from a cohort, $F$ is the fishing mortality (instantaneous rate) and $\bar{N}$ is the average number of survivors in that cohort. The same mathematical expression applies in the case of the number of deaths caused by natural causes including predation: $D = M\ \bar{N}$, where $D$ is number of fish which are dying from natural causes and $M$ is the natural mortality (instantaneous rate). $D$ is not observed directly, but it is assumed that an important proportion of fish that die from natural causes are eaten by other fish. This proportion can be calculated based on observations of predators' food and feeding rate.

Natural mortality is separated into two components $M = M_p + M_o$. MSVPA assumes that $M_o$ is a (small) constant while, $M_p$ is calculated from the estimated stock sizes and stomach contents. MSVPA calculates the number of prey species $k$ eaten by each predator $i$ as:

$$P_{ki} = M_{pki}\,\bar{N}_k \tag{29}$$

The model for $M_{pki}$ is based on the population size of prey and predators and on "suitabilities" ($U_{ki}$), which measure how suitable prey $k$ is as food for a predator $i$. These suitabilities are proportions and add up to 1 for each predator species. The MSVPA defines a "suitable food biomass" of prey $k$ for predator $i$ as $\bar{N}_k\, w_k\, U_{ki}$. Here, $w_k$ is the average body weight of prey species $k$. This quantity of suitable biomass is linked to the stomach content data by:

$$S_{ki} = \frac{\bar{N}_k\, w_k U_{ki}}{\sum_j \bar{N}_j\, w_j U_{ji}} \tag{30}$$

where $S_{ki}$ is the weight of prey $k$ in the stomach of predator $i$ as a proportion of the total weight of stomach contents of predator $i$. This is assumed to be equal to the suitable biomass of prey $k$ as a proportion of the total suitable biomass available to the predator.

Then finally introducing the total annual food consumption of each predator $i$ ($R_i$), we can calculate the total number of prey $k$ eaten by predator $i$:

$$P_{ki} = \frac{\bar{N}_i\, R_i\, S_{ki}}{w_k} \tag{31}$$

from which the predation part of the natural mortality can be calculated as:

$$M_{pki} = \frac{\overline{N_i}\, R_i\, U_{ki}}{\sum_j \overline{N}_j\, w_j\, U_{ji}} \tag{32}$$

and finally the total predation mortality is found by summing over all predators:

$$M_{pk} = \sum_i M_{pki} \tag{33}$$

The MSVPA assumes that food preference is well defined and remains constant between years. Therefore, it is possible to apply stomach content data from one period to the entire time series. This is equivalent to assuming that the suitabilities $U_{ki}$ are time independent.

The calculations for solving these sets of equations are organised as a functional iteration, but consist of two nested iterations. The inner iteration solves the catch equations for given $M$, i.e. find $F$ and $N$ in $C = F\,\overline{N} = F\,N\,\frac{1-e^{-F-M}}{F+M}$

The outer iteration finds $M_{pki}$. The procedure works year-by-year starting from the most recent year and progressing backwards in time. As opposed to the ordinary VPA, the calculations have to be done year-by-year rather than cohort-by-cohort.

In the calculation of $M_{pki}$, it is possible to calculate the suitabilities directly from the stomach content data and the average population sizes; the formula is

$$U_{ki} = \frac{S_{ki}/(\overline{N}_k\, w_k)}{\sum_{j \in prey} S_{ji}/(\overline{N}_j\, w_j)} \tag{34}$$

## 4.9 COMPARISON WITH OTHER STOCK ASSESSMENT MODELS

The cohort model is very similar to most other time series 'depletion model' techniques, such as the Leslie, Delury and Biomass Dynamics models. All these models rely on fishing to decrease the stock size, so that an index can be matched against removals of fish and the impact of fishing measured. Where catch-at-age methods do much better than these models, which describe entire undifferentiated populations, is that they remove the parameter confounding with recruitment (other than by assuming no recruitment). By following each age class, and assuming no immigration, a much better estimate can be obtained of fishing mortality even with little change in fishing effort.

VPA is closely related to other catch-at-age methods. Statistical catch-at-age methods, such as catch curves and Doubleday's (1976) method also rely on modelling cohort mortality in much the same way (as in the least-squares approach

of Section 4.7.3). The crucial difference is that in Doubleday's method the catches used in the population model are not the observed catches, but expected catches from the model itself. This has the effect of smoothing the population model through the data. A possible advantage is that the model can be fitted to data in its entire form. The disadvantage is that it may not take full account or advantage of perturbations induced by random changes in catches, so that this source of process error is not accounted for. An extreme example of the error this might incur is indicated by the fact that it is possible to fit statistical models where the cohort size is smaller than the observed catch, the difference being treated as "observation error". In VPA, this is not possible. This is not a disadvantage where catches are estimated and the error might be genuine. Then the issue becomes the relative weighting to give catch data over other data types.

# 5 LINK MODELS

Where variables, such as stock size, can be observed directly, the concept of link models is largely redundant. However they are useful where only indirect observations can be made on these variables, and the relationships are complex, as is almost always the case. Separating link models from the population model is useful in several respects. It allows a number of indices to be incorporated into the fitting process, each with their own separate model describing how they are related to variables in the population model. Ideally link models avoid any time series effects, as unlike population models they should not represent a process. This means the link models are subject only to direct measurement or observation errors. Finally, link models are often linear in form. This has a distinct advantage in that linear parameters, which can be estimated directly, are separated from non-linear parameters, associated with the population model, which need to be estimated iteratively. This can significantly decrease the time needed to fit the model.

Link models will always add information to the population models if the number of parameters is less than the number of data points. However, clearly the fewer the parameters in the link model, the more information there will be for fitting the population model. So a biomass survey, which requires no parameters, is preferable to a biomass index which requires at least one parameter. In some cases a large number of parameters are required to account for changes having nothing to do with the stock. This will undermine the value of the data series.

## 5.1 ABUNDANCE INDICES

### 5.1.1 Index Standardisation

For many indices there are a number of potential influences besides the variable we are interested in. For example, CPUE may be affected by the fishing area, season, gear, size of vessel, and number of crew as well as the stock size. Standardisation aims to separate these effects, in particular removing those that may bias the population size index, and to generate indices, which may be some of the fitted parameters. In order to be able to evaluate the quality of the index that is derived, a key statistic is the proportion of the variability that can be explained by the explanatory variables. This proportion is often quite low in these types of analysis, in the region of 50-60 %.

The analysis most often used is a special case of the generalized linear model approach (McCullagh and Nelder 1983). In the version applied in many fish stock assessments, the task is to find the variation in the data that can be allocated to vessel, time and area. This is done by applying a model of the form:

$$\ln(CPUE) = Constant + Vessel + Area + Year + Season + Area.Season \qquad (35)$$

where the "." operator refers to the interaction terms between factors (see McCullagh and Nelder 1983). In specific analyses, there may be fewer terms involved (e.g. if

only one vessel is used in the survey and if the survey is confined to a particular season throughout the time series the vessel and season terms do not appear).

The analysis provides an estimate of the value of the explanatory parameters. These parameter values are often used as input for the subsequent stock assessment. For example, the year effect in an analysis of CPUE data from an abundance survey could be used as an estimate of relative annual abundance and the vessel effect is the relative fishing power.

The season effect is often interpreted as either difference in availability – fish concentration varies with the season – or as seasonal migrations. The migrations should make the interaction term (area.season) significant (i.e. the geographical distribution of fish varies through the year).

In many fish stock assessments, it is preferable to isolate individual analyses and investigate the data in subsets. For example, studies of the structure of the catch data, the abundance CPUE data from surveys and CPUE data from logbooks can be undertaken separately. Only when one is satisfied with the consistency of the data does it make sense to include the data in an integrated model. For this purpose, linear models are often used (Gavaris 1988, Kimura 1981, Large 1992).

### 5.1.2 Dis-aggregated Abundance Indices

This is the class of indices most often used in fish stock assessment based on the VPA analytical model. These indices are typical CPUE estimates from either well-defined commercial fleets or from abundance surveys using research vessels. The CPUE values are expressed in numbers-by-age per effort unit. The effort unit can be days-at-sea, trawl hours, search time, etc. Commercial CPUE data are obtained through sampling the commercial fisheries for biological information and linking this information with catch and effort statistics. Abundance surveys using research vessels provide these data directly, often from bottom trawl surveys expressed as numbers caught per hour trawling.

Survey data differ from commercial CPUE data in two respects:

- Survey data are obtained through a designed sampling programme and the data often represent the stock over a short time period.

- Commercial CPUE data represent the geographical distribution of fishing activities as well as fish abundance, but the data often represent the stock over a longer time period.

Whether the CPUE data are linearly (or otherwise) related to abundance is discussed separately for the two data sources as the problems are distinct. For commercial fishing, the sampling is probably not random relative to the population and there are a variety of fishing vessels with different fishing strategies and different fishing power involved in construction of the mean CPUE value. Surveys represent few samples, the largest surveys include 500-600 trawl stations per year, but the coverage, effort allocation and standardisation of gear and fishing strategy are under the control of the researcher. In the models to be studied below we assume a linear relation between CPUE and stock abundance. Experience with non-linear models has shown

marked problems with over-estimation of stock size (and corresponding under-estimation of the fishing mortality), because of the random noise in the data.

#### *5.1.2.1 Commercial CPUE data*

Even when it is possible to dis-aggregate commercial CPUE data, they are often only representative for a time period, e.g. a quarter or a year. The link model becomes:

$$\ln CPUE_{ay} = \ln q_a + \ln \tilde{P}_{ay} \tag{36}$$

The population model might need to be corrected to match the population relevant for the CPUE index. The model must not only account for any mortality occurring in the population before the index is measured, but also for any mortality occurring in the stock over the time period for which the index measurements are taken:

$$\ln \tilde{P}_{ay} = \ln P_{ay} - \alpha Z_{ay} + \ln \frac{1-\exp(-(\beta-\alpha)Z_{ay})}{(\beta-\alpha)Z_{ay}}$$

with

$$Z_{ay} = F_{ay} + M_a \tag{37}$$

The constant $\alpha$ is the fraction of the total mortality that occurs before the index is relevant and $\beta$-$\alpha$ is the fraction of the mortality occurring while the index is relevant. In practice, these fractions are not known precisely and are approximated by the fraction of the year that has past prior to the measurement starting, while $\beta$-$\alpha$ refers to the period the observed CPUE applies.

The random noise is usually assumed to be log-normally distributed, but following Methot (1990) this may not be appropriate as the age composition is a mixture of a contribution of total catch – possibly log-normal – and the breakdown of this catch into age groups – possibly multinomial. The estimation is very similar to estimating the total catch in numbers. There is, however, an additional problem as the effort data available are usually the nominal effort. The efficiency of a nominal effort unit may well increase with time and the fishing strategy of a fleet may change with time (e.g. as a result of changes in the geographical distribution or abundance of the stock). These problems suggest that CPUE indices from commercial fisheries may only be applicable for shorter time periods.

Another approach could be to estimate the catch based on effort data and a linear link between effort and fishing mortality. For a set of terminal $F$'s, the cohort sizes are calculated back using the observed catches and the standard VPA methodology. Catches can then be estimated based on the cohort sizes at the beginning of each year and the effort. Hence, the expected catch becomes:

$$\ln C_{ay}^{\text{mod}} = \ln P_{ay} + \ln\left(\frac{1-e^{-q_a E_y - M_a}}{q_a E_y + M_a}\right) + \ln\left(q_a E_y\right) \tag{38}$$

This method has the distinct disadvantage that the link model is non-linear, but the errors may be better behaved than using a CPUE index, particularly if $F$ fluctuates

widely during the time series to values greater than 1.0 year$^{-1}$. Alternatively, the $F$'s calculated from the VPA may be fitted to the effort directly, which should be easier (see Section 5.2).

#### *5.1.2.2 Survey data*

These data are often the best stock size indicators available since such data should include sampling design to control and measure errors resulting from the stock distribution, gear design etc. The survey will not necessary take place at the start of the year and the CPUE therefore should be corrected for the mortality that takes place between the start of the year and the start of the survey. The survey often lasts a short period (e.g. a month). Even so it may be relevant to correct the survey CPUE for the mortality that takes place during the time of the survey and the model is therefore the same as that presented for the commercial CPUE data (Equation 37). Note, for surveys of short duration, where effectively $\beta$-$\alpha$ = $0$, the last term in the model becomes zero.

### 5.1.3 Biomass Indices

Biomass indices are usually provided from two different sources: from commercial fishing where CPUE data (catch weight per trip, or per day-at-sea, or per trawl hour, etc.) may be available from logbook or landing reports. Such data may or may not be accompanied by biological sampling. It is therefore not possible in all cases to break these data down by number and by age group. Another data source that provides biomass indices are egg- and larvae surveys that provide estimates of the spawning stock biomass.

The model linking the CPUE biomass index to the stock is:

$$\ln I_y^{\mathrm{mod}} = \ln\left( q \sum_a W_a \tilde{P}_{a,y} \right) \tag{39}$$

where the population, $\tilde{P}_{a,y}$, is the appropriate adjusted population corresponding to the CPUE (Equation 37). As, in this case, the age dependency is not estimable, the model is formulated with a single (average) catchability parameter.

Spawning stock biomass estimates from egg- and larvae surveys can be obtained either in absolute terms or as indices. For establishing the link between these observations and the spawning stock biomass calculated from the analytical age disaggregated model, it is necessary to include a new data item, the maturity ogive ($mat_{ay}$). This is an array of proportions, which gives the fraction of each age group in numbers that is mature at spawning time. This ogive probably varies between years and maturity data should therefore ideally be available by year. However, such data are often not collected routinely and then an average maturity ogive is used for a series of years. The expected spawning stock size index is calculated as:

$$\ln I_y^{\mathrm{mod}} = \ln\left( q \sum_a W_a \, mat_{ay} \, P_{ay} \, e^{-\alpha F_{ay} - \beta M_a} \right) \tag{40}$$

where $\alpha$ is the proportion of the fishing mortality and $\beta$ the proportion of the natural mortality that is exerted on the stock before spawning (i.e. proportion of the year between 1st January and spawning time). In this case the mean weights-at-age, $W_a$, should be those of the spawning stock, not of the total stock nor of the catch.

These indices are often assumed to be log-normally or normally distributed. The indices may not be estimated directly from the surveys, but result from separate analysis of the survey data (Pennington 1983, 1986).

## 5.2 FISHING MORTALITY INDICES

Effort data are often provided through fisheries statistics. These data can be collected from logbooks, from landing reports or as interview surveys of skippers. The model most often included in assessments is the assumption of a linear relation between fishing mortality and nominal effort:

$$\overline{F}_y = q E_y^{obs}$$

or in logarithmic form: (41)

$$\ln \overline{F}_y = \ln q + \ln E_y^{obs}$$

where the $\overline{F}_y$ is the average fishing mortality of the fully recruited age groups. There may well be data from several fleets each representing a different segment of the age composition of the stock. These fleet data may all be valid stock indicators that preferably should be included in the assessment.

Nominal effort may not be linearly related to the fishing mortality. This is because fishing is not a random sampling of the stock, but all possible skills are used to find those grounds where the catch rates are highest. Another problem with the use of such data is the increase in efficiency that takes place over the years. (Squires 1994, Pascoe and Robinson 1996). Such efficiency increase would be reflected by a time dependence in the catchability $q$.

In Section 4.4, a separable VPA model was introduced as part of the population model. However, it can also be developed as a link model. In this case, Equation 41 is expanded to allow for different catchabilities for each age group:

$$F_{ay} = q_a E_y^{obs} \quad (42)$$

We can then fit these estimated $F_{ay}$ to those in the VPA population model (Equation 7) given the terminal $F$'s (perhaps also derived from Equation 42). This approach assumes an error between the expected and observed fishing mortalities rather than catches, which may be considered more appropriate if catches are considered more accurate than nominal effort. Because both Equations 41 and 42 are linear, they usually add only a small cost to the fitting procedure (see Section 6.3 Finding the Least-squares Solution).

It should be noted that the effort data may already have been used to construct CPUE stock indices and in this case the effort data should not be used again as part of the estimation procedure.

## 5.3 USING LENGTH COMPOSITIONS

Although VPA methods use age, catch data is at best divided into size classes. The link between numbers-at-size and numbers-at-age is potentially a complex one. Therefore, this link is usually dealt with separately as a conversion from size to age frequency using a variety of different methods. Once the conversion is complete, the VPA proceeds as though all fish were aged.

There are several groups of species where it is not possible to age individuals, such as shrimps, nephrops, lobsters, crabs and many tropical fish species. Crustaceans do not possess bone structures that they keep throughout their life span and therefore their shells or exoskeletons cannot be used for ageing. The environment of tropical fish may not have sufficient seasonal differences to establish well-defined structures in otoliths and bones[1].

In these cases, the approach is to use solely the length compositions in the population as the basis for establishing cohorts. Reproduction, even in tropical areas usually shows some seasonal pattern (e.g. based on the local rainy season) and this is reflected in the length compositions where a peak in the length composition will identify a cohort.

In length-based assessment, we define a method that converts length composition into age composition without age data. This procedure is often called cohort slicing (the generic term). The basis of the procedure is to allocate an age to a proportion of the fish found in a length range. This is precisely what the ALK does with available size-age sample. The difference is that whereas ALK can identify different age groups among similarly sized fish, cohort slicing cannot, which may lead to inaccurate allocation of catches to cohorts.

Although we only use length in this discussion, other additional biological information might be used. In all cases, a good knowledge of the biology of the species being analysed can greatly assist in developing models. For example, it is possible to use the sex or location of capture of some species to assist in establishing the age structure.

The present discussion is an expansion of Lassen (1988). Several methods are implemented in the FAO/ICLARM software (Gayanilo Jr. *et al.* 1996). Common length based approaches are explained in Sparre and Venema (1998).

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1 This observation may very much depend on the species and local conditions. It may always be worthwhile exploring whether direct ageing techniques can be used for tropical fish for each fishery, as their use greatly enhances the scientific advice that can be given to help manage the fishery.

### 5.3.1 Factors Affecting Length Frequencies

Observed length frequencies depend on relative year class strength, total mortality, average growth and variation in growth. This is illustrated in the following examples where individual parameters are varied to produce simulated length frequencies. In each case, the effect of the parameter is illustrated with respect to interpreting length frequency distribution, and in particular identifying modes in these distributions representing individual cohorts.

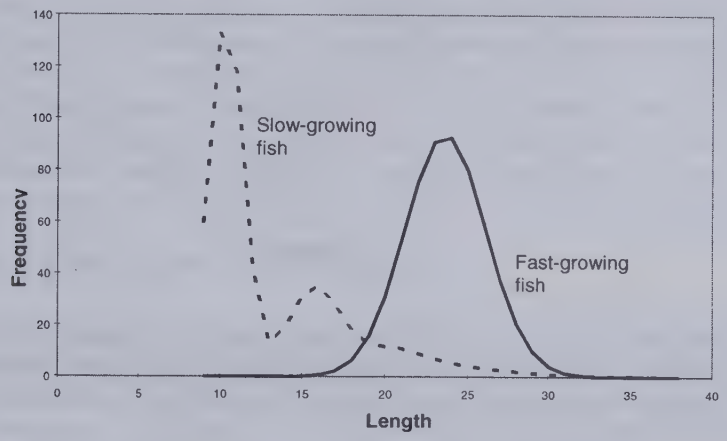


**Figure 5.1 Theoretical length distributions for two sets of growth parameters, with the same mortality (1.0 year$^{-1}$), for the Eastern Baltic cod fishery year classes 1966-1994. Modes representing cohorts can only be detected in the length frequencies for slow-growing fish.**

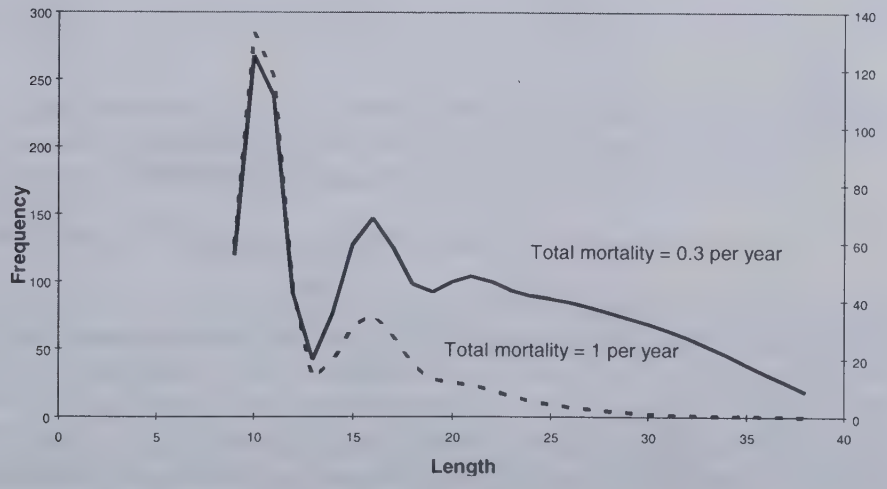


**Figure 5.2 Theoretical length distributions for slow-growing fish, with different mortalities. Lower mortality gives a greater chance of detecting modes for older cohorts if significant differences remain between sizes at these ages.**

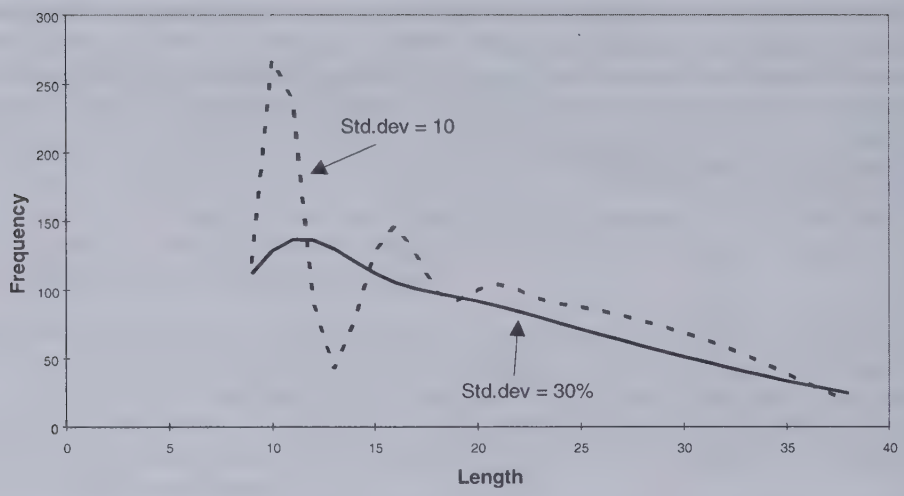


**Figure 5.3 Theoretical length distributions for the same set of growth parameters and mortality, but with two levels of variation in growth. As variation in growth increases it becomes more difficult to detect modes as cohorts merge in size frequency.**

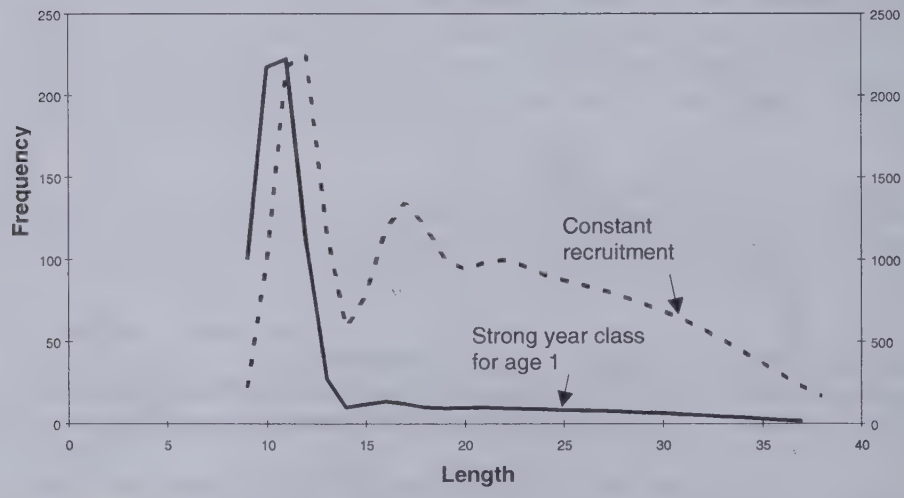


**Figure 5.4 Theoretical length distributions for the same set of growth parameters, mortality and growth variation, but with and without variable recruitment. Recruitment variability tends to mask modes of cohorts from weak recruitments. However tracing strong year classes through time may give indications of growth rates.**

The conclusion from the examples is that simple identification of peaks in the length frequencies can be impossible. It will work when there is low growth and recruitment variability, but otherwise no modes would be apparent. Analysis of a set of length frequencies under the assumption of common growth can help, as this will guide where the peaks are considered to be on the length axis. Such analysis, in many cases, is critically dependent on the growth assumption being correct.

### 5.3.2 Length to Age Conversion

There are three approaches to decomposing size groups into ages. Each method links observations such as age and size samples to catches in numbers per age class, which are the variables used in the population models. Notice that it is hardly ever the case that catch-at-age is observed directly. The preferred method is to use age data through age-length keys (ALKs). In tropical fisheries, there is often a heavy reliance on size frequency data only, which will incur a significant penalty in accuracy. Wherever possible, ageing should be considered as part of the data collection programme.

#### *5.3.2.1 Methods Using Age-Length Keys (ALK)*

Use of size frequencies can greatly enhance the use of ageing data, as ageing is generally expensive. Using size frequencies allows improved sampling techniques reducing the amount of ageing that needs to be done by making use of the information contained in fish size to help generate the age distribution. Unlike other methods it does not depend on size however, so even larger size groups can be broken down into age categories. All the usual sampling techniques apply. So, age samples should be stratified by size, but be random within each size group.

A link model can be used to define catches in each age group as a sum of catches from the size groups:

$$C_{ay} = \sum_{l} p_{la} C_{ly} \,. \tag{43}$$

where $p_{la}$ = the proportion (i.e. a probability) of fish in length group $l$ of being age $a$. The $p_{la}$ parameters can be estimated, for example, from age-at-length data using a multinomial model (McCullagh and Nelder 1983).

#### *5.3.2.2 Methods Not Requiring a Growth Model*

These methods rely on identifying modes in length frequency samples representing cohorts. For example, the Bhattacharya method uses the first mode in a sample to fit a normal curve representing the youngest cohort. This curve is then used to remove all fish belonging to this cohort from the sample. A similar procedure is then applied to the next mode, and so on. Methods include Bhattacharya (1967), Tanaka (1956), MIX: MacDonald and Pitcher (1979) and NormSep: Hasselblad and Tomlinson (1971).

### *5.3.2.3 Methods Requiring a Growth Model*

The simplest case is Jones length-based cohort analysis (Jones and Van Zalinge 1981). In this growth is assumed deterministic and the sample is sliced up according to back-transformation of the von Bertalanffy growth equation.

The method is based on re-writing the survival equation into length differences:

$$\Delta t = \frac{-\ln(\frac{L_\infty - l_1}{L_\infty - l_2})}{k} \text{ for each size class} \quad (44)$$

$$N_{l+\Delta l} = N_l e^{-Z\,\Delta t} \quad (45)$$

where $l_1$ and $l_2$ are respectively the lower and upper bounds of the size class. Note that size classes should be chosen such that $M\Delta t$ should be less than 0.3.

Given the change in age over each size class ($\Delta t$), the population sizes within each class can be constructed in much the same way as a VPA. The method requires that the growth parameters are known. Methods such as ELEFAN may be used to estimate these. Provided appropriate averaging of the length compositions has been done so that the observed length compositions can be assumed to present the equilibrium length compositions, then a simple VPA back-calculation over length rather than age groups is possible.

The method has been investigated (Addison 1989, ICES 1995a,b) with the following conclusions:

- Cohort analysis works on a single length frequency sample assuming the population has been in a steady state. A number of length frequency samples from different times may be required to verify this.
- The model is insensitive to errors in the terminal exploitation rate, if $F >> M$.
- The model is extremely sensitive to $M$.
- The narrowest length interval that makes data reasonably smooth should be used.
- Considerable care should be taken with the method when only poor growth data are available or when individual variation in growth is high. Ensure the terminal length interval ("plus" group) has an initial length (lower bound) of less than 70 % of $L_\infty$. This will minimise errors in the model's output due to errors in estimates and variances of $L_\infty$ and $k$. Any estimate of overall $F$ should therefore cover only the smaller size interval representing the majority of the catch.
- Estimates of abundance should not be taken as absolute values. Use them only as indices to reflect relative changes.

More realistically, other methods use the growth model (usually the von Bertalanffy model) to relate the age of a fish to a parameter of a probability distribution of its size. The parameter is usually taken to be a mean, and the probability distribution is the Normal. So given growth parameters, and some parameter summarising the variation in growth-at-age, we can define the probability ($\varphi$) a fish of length $l$ is age $a$ as:

$$l_{age} = L_\infty\left(1 - e^{-k(a-a_0)}\right)$$

and

$$\varphi(l;age) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(l-l_{age})^2}{2\sigma^2}} \qquad (46)$$

The cumulative normal distribution can then be used to calculate the proportions of each length group, which should be allocated to each age group ($p_{la}$ in Equation 43). Other distributions, such as the log-normal may be used and in many cases may be more appropriate (see Beyer and Lassen 1994).

There are many methods to fit this and other similar functions to modes through one or more length frequency samples. They ignore modes if they do not conform to the growth models. These methods are complicated, but software is widely available, such as ELEFAN (Pauly 1987), SCLR (Shepherd 1987), MULTIFAN (Fournier *et al.* 1990).

The conversion from length to age based only on length frequency is usually subject to a variance much higher than that obtained in age readings. Most worryingly, this uncertainty is not quantified allowing a researcher to overestimate the accuracy of their assessment. Decomposition of the length distribution into age groups is less precise than ageing directly, and therefore should be used only when no ageing methods are available.

# 6 ERROR MODELS AND ESTIMATION

Model specification usually includes a description of the behaviour of the mean in the distribution and a random effect or error. This error is the difference between the model expected value and the observed value, and can be classified as:

- **Structural error.** The estimation procedure uses structural relations between the populations at different times. These relations will only be approximately correct. For instance, CPUE is unlikely to be precisely proportional to abundance, although this model makes estimation easier.

- **Measurement error.** This error is not only caused by the sampling gear, (e.g. originating from variation in weather conditions during surveys), but also by patchy distributions of the population.

- **Process error.** Random effects may also affect underlying dynamics models. For instance, random weather and oceanographic changes may increase or decrease natural mortality and recruitment in an unpredictable way. The difference between process and measurement error is that process error introduces a real change in the system, whereas measurement errors introduce no underlying change and therefore do not affect future observations.

## 6.1 LIKELIHOOD

In fitting models to data, the models describing the stock and observations cease to become descriptions of the process in their own right, but instead become descriptions of how parameters in probability models change. For example, in many applications a model is used to describe the $\mu$ parameter in the normal distribution, which also happens to be the mean.

These probability models describe how likely the observed data are, given the parameters. The likelihood concept simply turns this on its head. Likelihood is the probability that a set of parameters is correct given the data. This makes no substantive difference to the probability distribution, but conceptually underpins most criteria for fitting models to data. For example, maximum likelihood defines a set of parameters when the likelihood function reaches its maximum point, and a Bayesian estimator uses likelihood, along with prior probabilities and a cost function, to define a set of parameters where the expected cost is minimised.

Although using likelihood (i.e. a full probability model) is theoretically better, least-squares is often used in the analysis of fisheries data. This can be justified by the following points:

- least-squares is maximum likelihood where the probability distribution is the Normal.

- true likelihoods can rarely be specified with any certainty. Least-squares with some appropriate transformation is probably as good as any alternative without

more information on error structure. Therefore, a more complex procedure may not be justified.

- maximum likelihood for many parametric likelihoods (e.g. Poisson etc.) can be reformulated in terms of least-squares.

- least-squares numerical procedures are much simpler and less likely to break down than more general approaches, particularly where there are many parameters to estimate.

The fact that least-squares are relatively easy to use, adaptable, objective and may often be close to the maximum likelihood solution has resulted in its wide use. Nevertheless, there is increasing interest in alternative approaches that are theoretically more appealing and for which robust numerical methods are being developed. However, even if other more complicated methods are used to fit models, in most cases least-squares can still form the starting point of the analysis, so the methods discussed here are always likely to be of use.

## 6.2 LEAST-SQUARES ESTIMATION

Least-squares estimation is based on the same principle as curve fitting. Given a set of observations, define a model and then establish the set of the parameters that gives the "best fit" of this model to the observed data. The "goodness of fit" is usually the sum of squared differences between observed and calculated dependent variables (i.e. squared residuals). The sum of squares (SSQ) is also sometimes called the Euclidean norm. The "best fit" is the set of parameters that minimises the squared difference between the observations and the model's expected values.

There is no guarantee that the "best fit" model is correct, and the model may be entirely inadequate for reflecting the dynamics. Analyses of a data set therefore should always include comparison between observations and the fitted model for inspection. This is often done graphically by plotting the residuals against the independent variables or by plotting on the same graph both the observations and the fitted curve. The residuals should show a random scatter and should not exhibit any remaining pattern.

Maximum likelihood estimation (e.g. Lehman 1983) includes the same elements as a least-squares estimation, only the goodness of fit measure will often differ based on the explicit assumption of the form of the error model.

The elements in least-squares estimation are:

The model: $y^{obs} = Model(\beta) + \varepsilon$ (47)

where $\beta$ is the vector of parameters, and $\varepsilon$ is the difference (error) between the observations and value calculated from the model. In practice, this means all uncertainty is treated as observation error whether created by measurement noise, model mis-specification or otherwise. The mean of the observed quantity can be defined as:

$$E\left\{y^{obs}\right\} = Model(estimated\ \beta) = Model(\overline{\beta}) \tag{48}$$

Therefore, the mean error becomes: $E\{\varepsilon\} = 0$. Where the expected error is not zero, this is often referred to as bias.

For the goodness of fit measure, the sum-of-squares, is used:

$$L = \sum_{obs} \left[y^{obs} - Model(\beta)\right]^2 \tag{49}$$

The parameters in the model are chosen so that this sum-of-squares is at its minimum. This goodness of fit measure is often extended to account for the observations having different variances. In this case, the goodness-of-fit measure becomes:

$$L = \sum_{i} \sum_{obs} \frac{\left[y_i^{obs} - Model(\beta)\right]^2}{\sigma_i^2} \tag{50}$$

where data subset $i$ contains all observations with the same variance $\sigma_i^2$.

A least-squares estimator will produce maximum likelihood estimates and confidence intervals if $\varepsilon = \varphi(0, \sigma^2)$, that is normally distributed with mean 0 and variance $\sigma^2$. It will even produce maximum likelihood estimates if the variance is constant over the range of explanatory variables or the proportional change in variance is known in a weighted least-squares scheme. However, if the true error distribution is not symmetrical, the variance changes in an unknown manner, or there are process or structural errors (as there almost certainly always are), the estimates will not be maximum likelihood.

It has been found with fisheries data that least-squares by itself provides a poor fit. For this reason, it is a common practice to use transformations to approximate alternative distributions. The transformations form part of the link model and often are used to represent alternative error distributions besides the normal. Elliott (1983) suggests the following transformations for stabilising the variance:

| Error distributions | Observation | Transformation |
|---|---|---|
| **Log-normal** | $y$: continuous | $ln\ (y)$ |
| **Poisson** | $y$: discrete | $1/y$ |
| **Binomial** | $h$: frequency | $2\ arcsin(\sqrt{h})$ |
| **General frequency distribution** | $h$: frequency | $ln(\ h/(1-h)\ )$ |
| **Taylor expansion** | $y$: discrete | $y^{\alpha}$ |

The most commonly assumed error is the log-normal, which is dealt with by taking logarithms of the data and then assuming that errors are Normally distributed. The use of the lognormal might be theoretically justified in some instances. For example, consider a cohort being subject to random survival rates between egg release and recruitment:

$$R_{\sum \Delta t} = R_0 e^{-\sum_i M_i \Delta t} \tag{51}$$

If the mortality is made up of a large sum of small random effects ($M_i$), the final total mortality, by the Central Limit Theorem, will be normally distributed even if the individual random components are not. Hence, this will result in a lognormal distribution.

As well as the practical observation that models fitted to log transformed data fit the data better, the log-normal has several other advantages:

- Taking logs often makes errors symmetrical around the mean. The Normal distribution does not discriminate against negative values, so for example, it allows for negative populations of fish, which are clearly impossible. In effect, this produces a bias towards larger observations in the analysis. The log-normal assumes negative values are impossible and corrects this bias. As a result, note that the exponent of the log-normal parameter, exp($\mu$), is not the same as the arithmetic mean, but lower as $\mu$ is the mean of the log values. The arithmetic mean will depend on both the log-mean ($\mu$) and the variance.

- The log-normal does not assume a constant error variance, but assumes the variance increases with the arithmetic mean. Again, this has generally been observed in fisheries data, where increasing catches and effort tends to produce greater variability. The log-normal corrects estimates for this effect.

Nevertheless, the main argument for the log-normal remains pragmatic. It represents the observed error distribution better than would the normal, producing better estimates. However, you should always check which transformation if any is appropriate for your data by examining model residuals. The fact that a procedure is widely used is not a justification for its use in any particular case.

The model for which we want to estimate the parameters, provides the mean in the unknown probability distribution. Hence, for example, CPUE might be modelled as:

$$\ln CPUE = \ln q + \ln P + \varepsilon \tag{52}$$

where $\varepsilon$ = measurement error.

Based on the above model we expect that the mean value, the logarithmic mean CPUE over many stations randomly spread out in the survey area, will be a linear function of the population $P$ and that this mean value can be measured without bias. The estimation equation becomes:

$$\sum_a \sum_y \left[\ln Catch_{ay}^{obs} - \ln Catch_{ay}^{\text{mod}}\right]^2 +$$
$$\sum_i \sum_a \sum_y \left[\ln Cpue_{iay}^{obs} - \ln Cpue_{iay}^{\text{mod}}\right]^2 + .... = MIN\{\text{model parameters}\} \quad (53)$$

where subscript $i$ = abundance index, $a$ = age and $y$ = year of the observation. Most often there are several "tuning" data series available. A basic feature of the ADAPTIVE framework (Chapter 8) is to sum these individual contributions as in Equation 53. It is the researcher's responsibility to build the estimation equations relevant for each individual stock assessment.

### 6.2.1 Weights

When there is more than one "tuning" time series available the data of the different series are usually not obtained with the same measurement variance. In this case, it is preferable to introduce a weighting of the data series, by specifying a weight parameter, $\lambda_i$, for each data series $i$. In theory, these weights should be the inverse of the variance of the measurements. Estimates of the true variances are often available from abundance survey data, but they are more difficult to estimate for data from the commercial fisheries. However, it is unnecessary to obtain the absolute weights, only relative weighting with respect to some primary data series.

In least-squares theory, the variances can be estimated from the sum-of-squares as:

$$\frac{\sum_{\text{obs}} \left[X^{\text{obs}} - X^{\text{mod}}\right]^2}{(n-p)} \quad (54)$$

where $n$ is the number of observations and $p$ is the number of parameters in the model (e.g. Lehmann 1983). It is not possible to estimate weights within the estimation procedure, only once the model is fitted. This is illustrated by a simple system with two "tuning" data series $CPUE_1$ and $CPUE_2$:

$$\sum_{\text{obs}} \left[\ln CPUE_1^{\text{obs}} - \ln CPUE_1^{\text{mod}}\right]^2 + \lambda \sum_{\text{obs}} \left[\ln CPUE_2^{\text{obs}} - \ln CPUE_2^{\text{mod}}\right]^2 = MIN \quad (55)$$

This sum-of-squares clearly has a minimum for $\lambda = 0$ ($\lambda \geq 0$), as this eliminates the second contribution to the sum of squares. Therefore, weights need to be treated as external variables estimated through some other means.

Extended Survivor Analysis (XSA) (Shepherd 1991; Darby and Flatman 1994) includes an internal weighting procedure, treating each age group and each data series separately. These weights are introduced in a double iteration inherent in the method. Details of this procedure are discussed in Section 8.3.

All data types above can be integrated in the combined estimation least-squares expression:

$$\sum_{a\in age}\sum_{y\in year}\left[\ln Catch_{ay}^{obs}-\ln Catch_{ay}^{\mathrm{mod}}\right]^2+$$

$$\sum_{i\in Abundance\ indices}\lambda_i^{CPUE}\sum_{a\in age}\sum_{y\in year}\left[\ln CPUE_{iay}^{obs}-\ln CPUE_{iay}^{\mathrm{mod}}\right]^2+$$

$$\sum_{i\in biomass\ indices}\lambda_i^{biomass}\sum_{y\in year}\left[\ln I_{iy}^{obs}-\ln I_{iy}^{\mathrm{mod}}\right]^2+ \tag{56}$$

$$\sum_{i\in effort\ indices}\lambda_i^{effort\ index}\sum_{y\in year}\left[\ln E_{iy}^{obs}-\ln E_{iy}^{\mathrm{mod}}\right]^2=MIN\{\text{model parameters}\}$$

where $\lambda_i$ are the weights applied to data series.

## 6.3 FINDING THE LEAST-SQUARES SOLUTION

Finding the least-squares solution is the common problem of finding the minimum for a function.

$$\sum_{obs}\left(y^{obs}-Model(\beta)\right)^2=MIN \tag{57}$$

This problem is converted into an equivalent problem of solving a set of simultaneous equations. In any function a minimum occurs where the partial differentials of the parameters are equal to zero, so:

$f(\beta)=MIN$ with respect to the set of $\beta$'s is equivalent to

$\frac{\partial f(\beta)}{\partial \beta_i}=0\ for\ i=1,2,...$

In least-squares, the function $f$ is the $\chi^2$ function (the sum-of-squares), and the parameters are the parameters of the model. Any numerical routine could be used to find a solution, and good robust routines exist. Why not just use the canned, black-box routines available in many software packages? The simple answer is no reason in many cases, and as long as the researcher checks such routines have successfully found the minimum, they are recommended. However, in some cases they are not adequate, particularly when the number of parameters is very large. Faster, more reliable and more accurate methods may be developed for a problem by considering the numerical solution yourself.

With large numbers of parameters, the N-dimensional parameter space can become very complex. Routines written for general functions can make no assumptions about those functions. They therefore tend to crawl around the parameter space very slowly to avoid overstepping the minimum. This may still not avoid missing the minimum and can take inordinate amounts of time. Routines to find the least-squares minimum take advantage of attributes of the $\chi^2$ function, increasing the chance of success and the speed at which the minimum is found.

Canned black box routines are also widely available for finding least-squares, so why is the detail of methodology given here? The reason is largely the same. The researcher can take advantage of their knowledge of the function (i.e. the stock assessment model) to increase the chance of success and speed of the method. Any canned routine would treat the stock assessment model as a single function. However, a researcher will often see how the function could be broken down into simpler components, each amenable to simpler analysis. As will be seen, this approach is used in XSA, where a simple linear regression to estimate parameters of the model linking the population to the CPUE index, so these parameters can be solved by a single calculation. The parameters belonging to the more complex non-linear model still need to be found through iteration, but the number of parameters has been greatly reduced.

### 6.3.1 Linear Models

On the face of it, linear models would be of little use in stock assessment as most realistic population models are non-linear. However, there are often linear components, which can be estimated separately. The advantages of dealing with linear parts separately is purely pragmatic. Linear parameters can be found by calculation rather than iterative numerical procedures, which speeds up model fitting.

Where the model is linear, the least-squares equations are linear as well and can be solved directly through calculation. The solution is obtained by solving the M simultaneous linear equations, where M is the number of parameters or independent $x$ variables. The solution of linear simultaneous equations is subject to standard linear algebra techniques. Assuming equal variances, we wish to find the solution to a set of M equations:

$$\frac{\partial L}{\partial \beta_i} = 0$$

where

$$L = \sum_{k=1}^{N} \left( y_k^{obs} - y_k^{\mathrm{mod}} \right)^2 \qquad (58)$$

$$y_k^{\mathrm{mod}} = \sum_{i=1}^{M} \beta_i x_{ik}$$

and there are M parameters and N data points. The set of differential equations can be found easily for a linear model:

$$\frac{\partial L}{\partial \beta_j} = -2 \sum_{k=1}^{N} \left( y_k^{obs} - y_k^{\mathrm{mod}} \right) \frac{\partial y_k^{\mathrm{mod}}}{\partial \beta_j}$$

$$\frac{\partial y_k^{\mathrm{mod}}}{\partial \beta_j} = x_{jk} \qquad (59)$$

$$\therefore \quad \frac{\partial L}{\partial \beta_j} = -2 \sum_{k=1}^{N} \left( x_{jk}\, y_k^{obs} - x_{jk} \sum_{i=1}^{M} \beta_i x_{ik} \right) = 0$$

So, now we have M equations in terms of the $x$ and $y$ data variables and the parameters $\{\beta\}$, each equation equal to zero. These are rearranged suitable for a matrix format:

$$\begin{Bmatrix} \sum_k x_{1k}x_{1k} & \sum_k x_{2k}x_{1k} & \cdots & \sum_k x_{Mk}x_{1k} \\ \sum_k x_{1k}x_{2k} & \sum_k x_{2k}x_{2k} & \cdots & \sum_k x_{Mk}x_{2k} \\ \vdots & \vdots & \ddots & \vdots \\ \sum_k x_{1k}x_{Mk} & \sum_k x_{2k}x_{Mk} & \cdots & \sum_k x_{Mk}x_{Mk} \end{Bmatrix} \begin{Bmatrix} \beta_1 \\ \beta_2 \\ \vdots \\ \beta_M \end{Bmatrix} = \begin{Bmatrix} \sum_k y_1 x_{1k} \\ \sum_k y_k x_{2k} \\ \vdots \\ \sum_k y_k x_{Mk} \end{Bmatrix} \quad (60)$$

All the terms in Equation 59 now appear in Equation 60, but arranged as matrices. The solution for $\beta_i$ is conceptually simple. We multiply both sides of Equation 60 by the inverted matrix appearing on the left-hand side, isolating the $\{\beta\}$ vector. Reintroducing the variances for completeness, the solution can be written:

$$\{\beta\}_j = \sum_{i=1}^{M} \left[ \left\{ \sum_{k=1}^{N} \frac{x_{jk}x_{ik}}{\sigma_k^2} \right\}_{ij}^{-1} \left\{ \sum_{k=1}^{N} \frac{y_k x_{ik}}{\sigma_i^2} \right\}_i \right] \quad (61)$$

The $\sigma^2_i$ is the variance associated with each data point, and often is assumed equal among data points. This matrix equation allows the least-squares estimate to be obtained in one iteration.

The advantage of linear models should now be apparent, and occurs because differentiation eliminates the parameter from the equation, enabling the linearity of the equations to be maintained. This allows an 'easy' solution. With non-linear models, the set of Equations 59 will not be linear, and therefore no simple solution exists.

In the simplest case with only one parameter, Equation 61 becomes:

$$\beta = \frac{\sum_{k=1}^{N} \frac{y_k x_k}{\sigma_k^2}}{\sum_{k=1}^{N} \frac{x_k^2}{\sigma_k^2}} \quad (62)$$

If the $\sigma^2_i$ are constant among data points this equation becomes the sum of the product of the $y$ and $x$ variables divided by the sum of squares of the $x$ variable. This result is often very useful in estimating parameters in models linking observed variables to underlying population dynamics variables. For example, consider the case where we have generated a population time series from a model, and we wish to relate it to a CPUE index which requires estimating a single parameter $q$, as:

$$CPUE_t = qP_t + \varepsilon \quad (63)$$

Assuming least-squares, constant variance and time independent errors, $q$ can be calculated as:

$$q = \frac{\sum_{t=1}^{T} CPUE_t P_t}{\sum_{t=1}^{T} P_t^2} \tag{64}$$

This avoids the need to estimate $q$ as part of the minimisation process. Instead $q$ is calculated each cycle, and the numerical routine concentrates on solving the non-linear parameters associated with the population model.

A similar simple procedure can be undertaken with two parameters. In this case, we try to fit the logarithm of the CPUE to the log population size, assuming a non-linear relationship:

$$\begin{aligned} CPUE_t &= qP_t^v \\ \ln CPUE_t &= \ln q + v \ln P_t \end{aligned} \tag{65}$$

In this case, the parameter $v$ is the slope, but we also have an intercept parameter ($\ln q$). In the linear framework, constant parameters (non-covariates are often called factors) are estimated using dummy variables. Dummy variables take on values of 1 or 0 depending on whether the parameter applies to any particular observation or not. In this case, the constant applies to all observations, so the first x variable is always 1:

$$\begin{aligned} &y_t^{obs} = \beta_1 x_{1t} + \beta_2 x_{2t} \\ &\text{where} \\ &y_t^{obs} = \ln CPUE_t \\ &x_{1t} = 1, \quad x_{2t} = \ln P_t \\ &\beta_1 = \ln q, \quad \beta_2 = v \end{aligned} \tag{66}$$

Solving for $\beta_1$ and $\beta_2$ using the general Equation 61 gives:

$$\begin{aligned} \beta_1 &= \frac{S_{22}S_{y1} - S_{12}S_{y2}}{S_{11}S_{22} - S_{12}S_{21}} \\ \beta_2 &= \frac{S_{11}S_{y2} - S_{21}S_{y1}}{S_{11}S_{22} - S_{12}S_{21}} \end{aligned} \tag{67}$$

where

$$S_{11} = \sum_{t=1}^{T} (x_{1t})^2 = T$$

$$S_{22} = \sum_{t=1}^{T} (x_{2t})^2$$

$$S_{12} = S_{21} = \sum_{t=1}^{T} x_{1t} x_{2t} = \sum_{t=1}^{T} x_{2t} \qquad (68)$$

$$S_{y1} = \sum_{t=1}^{T} x_{1t} y_t = \sum_{t=1}^{T} y_t$$

$$S_{y2} = \sum_{t=1}^{T} x_{2t} y_t$$

Notice that the subscripts refer to the elements of the matrices and vectors in Equation 60. $S_{11}$ is the element in the first row and first column of the matrix on the left-hand side, and $S_{y1}$ is the element in the first row of the vector on the right-hand side. For two parameters, the matrix inversion is very simple and it is possible to write out the result in a simple equation as above. This simplicity rapidly disappears with larger matrices. Inversion is closely related to calculating determinants, which is a sum involving all row-column combinations of elements. For large matrices these calculations are not trivial and may take a considerable amount of time, although the method remains faster (or at least more exact) than its non-linear cousin.

A second problem with inverting the matrix, is it may be singular. This may occur through aliasing, or high correlations pushing the inversion calculations beyond the computer's precision. An alternative solution to removing the offending parts of the model is to use matrix transformation techniques, notably Singular Value Decomposition (SVD). These techniques do not produce different results, merely skirt around singularity problems (Press *et al.* 1989). However, a detailed description falls beyond the scope of this manual.

This technique, of estimating linear parameters separate from the iterative fit, is widely used, in XSA for example. The benefits should not be underestimated. Searches for the minimum of non-linear functions is not trivial where there are large numbers of parameters and any method that reduces this number should be used.

### 6.3.2 Non-linear Models

A usual approach to finding the minimum is the Newton iteration scheme:

$$\beta_i^{new} = \beta_i^{old} - \{H\}_{ij}^{-1} \left\{ \frac{\partial L(\beta^{old})}{\partial \beta_i} \right\}_i$$

where (69)

$$\{H\}_{ij} = \left\{ \frac{\partial^2 L}{\partial \beta_i \, \partial \beta_j} \right\}_{ij}$$

$\{H\}_{ij}^{-1}$ is the inverse matrix of second partial derivatives of the sum of squares with respect to parameter pairs, often called the Hessian matrix.

As in the linear case, the aim is to find the point where the simultaneous partial derivative equations are zero. This approach to minimisation works on the principle that the step length moving parameters towards the zero point should be ratio of the differential to the slope of the differential (i.e. the second derivative) at the current position, which will produce a the correct step length where the model is linear. On each iteration, $\{\beta\}_i^{new}$ is generated and becomes the $\{\beta\}_i^{old}$ for the next cycle, so eventually $\{\beta\}_i^{new}$ converges to $\{\beta\}_i^{old}$ and the iterations can stop. The starting point for $\{\beta\}_i$ is important, but reasonable estimates are often available in VPA applications (e.g. $F$=0.5 year$^{-1}$).

It is only for a few problems when the second order derivatives are actually evaluated analytically. Instead computer-oriented methods are based on numerical approximations to the first and the second order derivatives, which are based on calculations of the function at small departures ($h$), e.g.

$$\frac{\partial L(\beta)}{\partial \beta_i} \cong \frac{L(\beta_i + h_i) - L(\beta)}{h_i} = \varphi_i \tag{70}$$

defines the first derivative and

$$\frac{\partial^2 L}{\partial \beta_i \partial \beta_j} \cong \frac{L(\beta_i + h_i, \beta_j + h_j) - L(\beta_i + h_i, \beta_j) - L(\beta_i, \beta_j + h_j) + L(\beta_i, \beta_j)}{h_i h_j} = H_{ij} \tag{71}$$

defines the second derivative and could therefore be used to calculate the Hessian matrix, $\{H\}_{ij}$. More sophisticated methods are usually used as these calculations may not be accurate (see Abramowich and Stegun 1966). An actual application will very often use standard implementations (see Press *et al.* 1989), which work with all but the most ill-behaved functions. However, we can take particular advantage of what is known about the least-squares function to improve both the speed and chance of success in finding the minimum.

The minimisation problem is first converted into the normal equations. Because the sum of squares is at a minimum point, we know that:

$$\frac{\partial L(\beta)}{\partial \beta_i} = -2 \sum_{obs} \left[ y^{obs} - Model(\beta) \right] \frac{\partial Model(\beta)}{\partial \beta_i} = 0 \quad \text{for i} = 1,2,...,\text{p} \tag{72}$$

Likewise, explicit differentiation to produce the Hessian terms gives:

$$\begin{aligned} \frac{\partial^2 L(\beta)}{\partial \beta_i \, \partial \beta_j} = & -2 \sum_{obs} \left( y^{obs} - Model(\beta) \right) \frac{\partial^2 Model(\beta)}{\partial \beta_i \, \partial \beta_j} \\ & +2 \sum_{obs} \frac{\partial Model(\beta)}{\partial \beta_i} \frac{\partial Model(\beta)}{\partial \beta_j} \end{aligned} \tag{73}$$

The first term in Equation 73 containing the second partial derivative is generally ignored in estimating the Hessian matrix for two reasons. Firstly, the second derivatives are often small compared to the first derivatives (they are zero in linear models for example), so their inclusion may not improve the efficiency of the fitting. Secondly, in practice the first term will sum to a small value when $Model(\beta)$ estimates are close to the expected value of the $y^{obs}$ (i.e. the mean). Therefore, the procedure may be most efficient when the initial estimates are reasonably close to the best-fit estimates. The fitting process now becomes:

$$\{\beta\}_i^{new} = \{\beta\}_i^{old} - \left\{\sum_{k=1}^{N} \frac{\partial Model(\beta)}{\partial \beta_i} \frac{\partial Model(\beta)}{\partial \beta_j}\right\}_{ij}^{-1} \left\{\frac{\partial Model(\beta)}{\partial \beta_i}\right\}_i \quad (74)$$

In some cases, the Hessian in this form may be easy to obtain analytically. For example, notice that where the model is linear, the Hessian matrix is the same as that in Equation 60. Using the true differentials should improve the efficiency of the fit. In other cases, Equation 74 will not help as the first derivative is just too complicated to derive and simple numerical methods (e.g. Equation 70) are instead used to generate both the Hessian matrix and vector of first derivatives.

The scheme proposed in Press *et al.* (1989) is the Levenberg-Marquardt method, which uses either the Hessian matrix or a simple step routine where the Hessian is a poor approximation to the shape of the $\chi^2$ function. While it may not be worthwhile pursuing the analytical approach, some analysis may help in understanding the behaviour of the model and potential pitfalls in attempting to find the least-squares solution numerically.

## 6.4 ESTIMABLE PARAMETERS

While it is possible to formulate a least-squares function for any model it does not follow that all parameters can be estimated. This can be inherent in the model formulation or it can be because of a lack of sufficient information.

An example of a model that cannot be fully identified is where parameters multiply or add together in a way that cannot be separated by the data collected, such as $Model(\beta)=\beta_1 \beta_2 x$, where only the product of the two parameters can be estimated. In fishery biology, an example is the population equation:

$$N_{a+1,y+1} = N_{ay} e^{-M_a - F_{ay}} \quad (75)$$

The equation contains such a problem in parameters $F_{ay}$ and $M_a$ unless data can be brought to bear to estimate these parameters separately. It is this basic problem that explains the minimum data requirement for an analytical assessment. To separate the two, the catch in numbers by age and by year combined with observations on either the fishing mortality or the stock in numbers are required. Usually $M_a$ is just fixed as an external parameter.

It is not only the model structure that makes certain parameters inestimable. The data structure can also have features that prevent the estimation of all parameters.

This is the collinearity problem, indicated by high parameter correlation estimates. In extreme cases, parameters may be "aliased" which implies the data are inadequate to provide separate parameter estimates.

A simple example where such correlation occurs is in estimating fishing power based on vessel characteristics. Most characteristics are dictated by vessel size. So the size of net, vessel speed, hold size, number of crew, sophistication of gear all relate back to the size of vessel. In essence, because we do not have observations on catch rates of large vessels with small engines or small vessels with large engines, it is not possible to separate the effects of engine size and vessel length. What appears to be a large amount of data, all the different characteristics of the fleet, boils down to very little real information to separate vessels. Methods such as principle components analysis should be used to reduce a large number of correlated variables into a few representative uncorrelated components for this type of analysis.

A more worrying example for stock assessment is the possible relationship between stock size and catchability. Vessels aggregate in areas where catchability is highest. Fish aggregate to improve spawning success and minimise their natural mortality. There are several cases where it is suspected that as the population decreases, fish density on the fishing grounds remains constant, so effectively catchability is increasing as the population falls.

While correlations in linear models are relatively straightforward, it is much more complicated in non-linear models such as those used in fish stock assessment. It is not clear how terminal cohort sizes might be correlated with catchability estimates for CPUE indices before doing a full analysis.

Statistical experimental design ensures that such collinearity does not occur in experimental data. However in fisheries or oceanographic surveys, the researcher does not have the same degree of control over the system under investigation and such data, because of the oceanographic or biological links occurring in nature, often show some degree of correlation between the independent variables.

## 6.5 ROBUST REGRESSION

An alternative approach to least-squares is to apply "robust regression" (e.g. see Chen and Paloheimo 1995). The least-squares fit is based on minimising the squared sum of residuals and this sum can be strongly dependent on a few outliers (cf. the example above). Robust regression exists in different forms, but is based on either replacing the sum of squares of the residuals by some other measure of "goodness of fit", (e.g. the median) or ignoring a certain percentage of the largest residuals in the fitting procedure (trimmed LSQ). Using the median, the least-squares problem is reformulated to finding the best curve where 50% of the observations have positive and 50% negative residuals. Obviously the magnitude of the residuals is of no importance and therefore outliers have less influence on the final result than when normal least-squares is applied. The approach can be formulated based on fitting a model as:

$$Median\left\{(y_i - Model(\beta_i))^2\right\} i = 1,2,.... \qquad (76)$$

## 6.6 CATCH

In many applications catch errors are either ignored (e.g. in most ADAPT and XSA methods) or the errors are assumed to be log-normal (e.g. in the ICA or in the CAGEAN methods). The reason for ignoring these errors in the catch data is that the stochastic error in the catch data is often insignificant compared to the noise in the survey data. This is probably correct in many fish stock assessments, but only for the more abundant age groups. The number of old fish caught, if constituting only a few percent of the total catch, is unlikely to be precisely estimated.

Methot (1990) suggested as part of his "Synthetic Model" that the error structure of the catch data be decomposed into two contributions:

- Estimate of the overall catch in weight
- Estimate of the age composition

The first contribution can be assumed to have lognormal errors. For the second contribution, Methot (1990) suggests that a multinomial distribution is more appropriate. The estimation of the catch in numbers, $C$, is often obtained through a fisheries statistics programme that provides total landings by species and by time period supplemented by a biological sampling programme that takes a length sample ($n_l$) and an age-length key ($m_{la}$) (ALK). The estimation of the catch-at-age for the population model is:

$$C_a = C_\bullet \sum_l \frac{n_l}{n_\bullet} \frac{m_{la}}{m_{l\bullet}} \tag{77}$$

where the dot subscript indicates summation over that subscript (Lewy and Lassen 1997).

However, where the observed and expected catch is included as part of the sum-of-squares, we can use the age composition observations directly. In the simple case, the age distribution is a random sample of the catches with observed frequencies in numbers of fish, $h_{ay}$. The catch composition in the model is given by:

$$\Theta_{ay} = \frac{C_{ay}^{\text{mod}}}{C_{\bullet y}^{\text{mod}}}$$

$$\text{where} \quad \sum_a C_{ay}^{\text{mod}} = C_{\bullet y}^{\text{mod}} \qquad \therefore \sum_a \Theta_{ay} = 1 \tag{78}$$

Therefore $\Theta_{ay}$ is essentially independent of the total catch. In this case, the catch term contribution:

$$\sum_a \sum_y \left[ \ln C_{ay}^{obs} - \ln C_{ay}^{\text{mod}} \right]^2 \tag{79}$$

with the multinomial likelihood becomes:

$$\sum_{y}\left[\ln C_{\bullet y}^{obs} - \ln C_{\bullet y}^{\mathrm{mod}}\right]^2 + \sum_{a,y} h_{ay} \ln \Theta_{ay} + .... = MIN\{\text{model parameters}\} \tag{80}$$

Fortunately, because only the age sample, but not the catches, appear with the $\Theta_{ay}$ parameters, they can be estimated independently of the catch data and population model by finding the maximum of the multinomial likelihood function. Combining length sampling with ALK gives a similar result, but the formulae are more complicated (Lewy and Lassen 1997).

The variance can be found as:

$$\frac{Var(C_a)}{C_a^2} = \frac{Var(C_\bullet)}{C_\bullet^2} + \frac{Var(h_a)}{h_a^2} \tag{81}$$

for the simple situation when the age sample is a random sample of the catch. If it can be assumed that the variance contribution from the total landings can be neglected compared to the error due to ageing, and if the ageing error can be approximated by a multinomial distribution, then this can be simplified to:

$$Var(C_{ay}) \cong \frac{1}{n}\frac{C_{ay}}{C_{\bullet y}}\left(1-\frac{C_{ay}}{C_{\bullet y}}\right) \Bigg/ \left(\frac{C_{ay}}{C_{\bullet y}}\right)^2 = \frac{1}{n}\frac{1-\dfrac{C_{ay}}{C_{\bullet y}}}{\dfrac{C_{ay}}{C_{\bullet y}}} \tag{82}$$

where $n$ is the number of fish in the sample.

# 7 ASSESSING RELIABILITY

## 7.1 SENSITIVITY ANALYSIS AND THE EFFECT OF HIGHLY INFLUENTIAL OBSERVATIONS

The estimates of different parameters are not equally sensitive to all observations. A 10% change in an observation does not affect all elements of the estimated stock status equally. This is explored in sensitivity analysis. Sensitivity analysis in fish stock assessment is usually used in two contexts:

- Exploring how a change in an observation, e.g. a survey result, affects the estimate of the elements in the stock status.
- Exploring how a change in a parameter, e.g. the natural mortality will affect both the estimates and the projection of the stock.

The sensitivity of a function is defined as $\frac{\partial \log y(\beta)}{\partial \log \beta}$. This is the expression for the relative change of the function $y(\beta)$ from a relative change in the independent variable $\beta$ that follows from the identity $\frac{\partial \log y(\beta)}{\partial \log \beta} = \frac{\partial y(\beta)/y(\beta)}{\partial \beta / \beta}$.

The sensitivity can be calculated numerically by introducing small changes in the observations and re-estimating the parameters. The sensitivity of a stock projection is estimated following the same procedure: a small change in parameters or variables is introduced and the changes in an output quantity (e.g. the projected catch) is calculated and expressed relative to the introduced change. In order not to lose the overview of the sensitivity structure, some strategy for the observation change should be worked out before embarking on such studies. The above definition of sensitivity is then used to present the results.

It is of particular importance that observations that strongly influence the estimated parameters or the projections are identified. It follows in some cases directly from inspection of the data model, which are the most influential observations. For example, the estimate of the strength of the most recent year class will most strongly depend on the most recent survey result.

The influence of observations is assessed by alternately excluding each observation and repeating the estimation each time. When it is an abundance index that is under suspicion, removal is simple. Just ignore the contribution to the sum-of-squares from that index or from that year, and then revised estimates can be compared to those obtained with the full data set. If it is catch data that are suspected to be highly influential (e.g. for a particular year), the procedure will be to treat this as a year for which catch data were not available using the methods discussed in Section 7.4.

Robust regression tries to minimise these effects using lower weighting of observations with the largest residuals. This includes trimmed means regression,

where a proportion of the largest residuals are excluded from the estimation (see Section 6.5).

## 7.2 THE ANALYTICAL APPROACH TO VARIANCE-COVARIANCE ESTIMATION

An analytical estimate of the variance-covariance matrix can be obtained using calculus. The result can be obtained because at the least-squares minimum, the differential of the model with respect to each parameter is zero, and because overall variance can be estimated directly from the sum of squares calculated during the least-squares procedure. The analytical approach is only valid if errors are normally distributed. If it is suspected that they are not normally distributed then a more robust scheme is recommended.

From least-squares theory, the covariance matrix of the parameters can be defined as:

$$V(\beta) = 0.5\frac{L(\beta)}{n-p}\{H\}^{-1} \tag{83}$$

where $\beta$ is the vector of best-fit parameters, $\{H\}^{-1}$ is the inverse Hessian matrix (Equation 74) and $L(\beta)$ is the sum of squares, so $L(\beta)/(n-p)$ is the unbiased estimate of the error variance. As in Equation 74, the Hessian can either be approximated numerically or by partial differential of the model with respect to each parameter, so:

$$V(\beta_i, \beta_j) = \frac{L(\overline{\beta})}{n-p}\left\{\sum_{obs}\left(\frac{\partial Model(\beta)}{\partial \beta_i}\frac{\partial Model(\beta)}{\partial \beta_j}\right)\right\}^{-1}_{i,j} \tag{84}$$

While these estimates of the parameter standard error can be used to estimate confidence intervals, the procedure only works when errors are normally distributed, otherwise they are only generally indicative of the variation and correlation in parameters. For confidence regions, more robust techniques such as bootstrapping are much preferred.

## 7.3 ESTIMATING CONFIDENCE INTERVALS USING BOOTSTRAPS

Bootstrapping techniques are also known as "resampling" techniques or "computer intensive" methods (Efron and Tibshirani 1993, Manly 1996). Manly (1996) distinguished between these concepts and defines re-sampling as sampling without replacements, bootstrapping as sampling with replacement and Monte Carlo methods as the generation of random number from a specified theoretical distribution. We restrict our discussion to the sampling with replacement technique, but also note that in many applications other techniques may be extremely useful.

Bootstrapping is based on the idea that the observations are a random sample from the population under investigation and any random sample from the observations

also forms a random sample of the population. A simple example of the procedure is illustrated by a linear regression between two covariates. In this simple case, the observations are the paired control and response variables. The procedure is implemented as:

(i) List the observations and number them 1,2, ... $n$.

(ii) Using a random number generator (or table) select a sub-sample with $k$ elements using sampling with replacement. In many applications, the size of the sub-sample $k$ is chosen to be equal to the total number of observations in the original sample $n$.

(iii) Calculate the statistics under investigation, in this case slope and intercept of the regression, and store the results.

(iv) Repeat the calculations from point (ii) above 100 to 1000 times, depending on the specific problem and the accuracy needed.

(v) When enough estimates have been obtained, appropriate statistics can be calculated, typically the mean, variance and 10%, 50% and 90% percentiles. These statistics are indicative of the properties of the estimated parameters.

This procedure works fine and is very robust to model structural errors, unless the observations are dependent. In fisheries models, the sequential dependence between observations forms part of the population dynamics, so this procedure often cannot be used. The alternative approach is to use the fitted model and residuals. Each observation is made up of the model estimate and the residual error. If each of the model estimates are combined with residuals drawn randomly with replacement, a new simulated data set is created. The procedure now becomes:

(i) Fit the model and obtain expected values for observations, and calculate the residuals.

(ii) Using a random number generator (or table) add to each expected value a new residual drawn at random with replacement to create a new simulated observation.

(iii) Fit the model to the new simulated data.

(iv) Calculate the statistics under investigation (in the case of fisheries, fishing mortalities, selectivity etc.) and store the results.

(v) Repeat the calculations from point (ii) 100 to 1000 times, depending on the specific problem and the accuracy needed.

(vi) When enough estimates have been obtained, appropriate statistics can be calculated, typically the mean, variance and 10%, 50% and 90% percentiles.

It is critical before applying bootstrap procedures to have a good understanding of the error structure. Bootstrapping aims to simulate these errors, so the procedure should follow the correct error model as far as possible. For example, if we have two CPUE time series, we may not want to assume that they have the same error

distribution. In this case, the residuals from which each new series is generated are kept separate. The case is a little more complicated if the variance is thought to change during the series. Although it may still be possible to draw random residuals, they will have to be re-scaled according to the estimated variance of each observation.

The real advantage of the bootstrap scheme comes when we need to estimate the parameter variation associated with a complex estimation procedure. It is not unusual to apply sequential analyses for fisheries. For example, we might firstly estimate a growth rate parameter from size frequency data before using that same data to slice catches into cohorts and apply VPA. We can apply the bootstrap procedure in this case by simulating the length frequency sample and catches, and then use these data to estimate the growth rate, cohorts and so on right through the procedure as though on real data. As long as the whole procedure is repeated enough times and the assumptions underlying the errors and models are correct, the estimates of uncertainty should also be correct.

In some cases, the error model is too complex to use real residuals, or perhaps more often the sample size is too small. In these cases, we may use the data to estimate the parameters of an assumed error distribution rather than use observed residuals. Errors are then drawn from this parametric distribution, rather than the set of residuals. This obviously requires an additional assumption on the exact nature of the error distribution, but is preferable to using only a small sample of residuals.

## 7.4 ESTIMATION WHEN DATA ARE MISSING

It is not always the case that time series data are complete. The estimation of stock status is still possible, but the lack of data means the variance of the estimates increases. There is no problem if there is a year without an abundance index, it is simply left out of the sum-of-squares. It is a little more difficult if catch data are missing. Most VPA methods require that a cohort can be fully traced without gaps in the time series. The virtual population is actually the sum of all catches of a given cohort and this represents a lower bound on the original recruitment.

Where observations are not independent, so they cannot just be excluded (i.e. mainly data used in the population model), the general approach is to use the expected value in place of an observation. The iterative procedure of replacing missing values with their expected values from the model and then refitting the model to generate new expected values until convergence, is known as the EM algorithm. The algorithm is robust, but can be very slow.

Similar procedures have been proposed on the basis that the stock and fishing mortality can be calculated from:

$$N_{ay} = Cpue_{ay} / q_a$$

and (85)

$$F_{ay} = \ln\left(\frac{Cpue_{ay} / q_a}{Cpue_{a+1,y+1} / q_{a+1}}\right) - M_a$$

Which give the expected catch based on the Baranov equation (7). Calculating the expected catch in this way can be built into the estimation procedures for those years when the catch data were not available or unreliable. A simple approach is to use the above equations to derive the catches for the year(s) when data were not available, complete the catch-at-age and year matrix with these data and perform the parameter estimation, but exclude these "data" from the model fit (see also Patterson 1998b).

If the separability model applies (Equation 11), the problem reduces to the estimation of the exploitation level $E_y$ for the year for which catch data are missing. In that case the simpler solution is to ignore the contribution to the sum-of-squares from the year for which the catch data are missing and fit the E(y) array as in the standard procedure.

If the total catches are available, but there is no age information for a specific year then the age-length keys must be interpolated between years (Hoenig and Heisey 1987). This is built on estimates of growth and recruitment for the stock in question. For those length groups where the recruiting year-class overlaps significantly with older fish, the ALK becomes very uncertain. Fortunately, such overlaps do not occur frequently. The procedure most often used, simply applying an average ALK or the ALK of the previous or next year, can lead to quite large errors in the estimated mortality. These procedures should be used with caution.

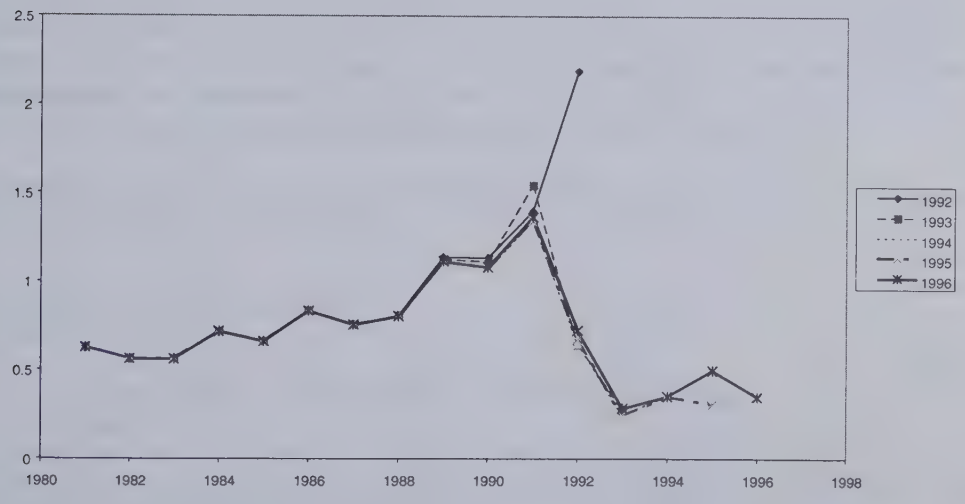


**Figure 7.1 Retrospective analysis on $F$ for age group 4 eastern Baltic cod. Each analyses uses one more year's data: 1981-1992, 1981-1993,..., 1981-1996. It is apparent that the estimate for 1992 when that was the final year in the analysis was inaccurate. Otherwise, the estimate of the fishing mortality for the most recent year seems to be stable. Although in 1995, there was some change after the 1996 data were added.**

## 7.5 RETROSPECTIVE ANALYSIS

The idea behind retrospective analysis is very simple. Drop one or several of the most recent years' data, repeat the analysis and compare with the analysis including those data (Figure 7.1). The analysis will identify years, which lead to poor projections and test the models general capability of prediction.

An alternative approach to retrospective analysis is to restrict the data to, say, 10 years and estimate the stock status based on such a moving window across the data. The results will not differ significantly particularly as one is most interested in the behaviour of the estimate for the most recent year.

Retrospective analyses have been used extensively to investigate the performance of particular assessments. For example, it is part of the standard ICES assessment procedure.

# 8 ADAPT

The data model of ADAPT supplements the catch in numbers-at-age and year with at least one abundance or biomass index series. This allows estimation of the entire set of equations. With the exception of natural mortality, this leaves no external parameters to be fixed, as VPA requires. Care should be taken that there is sufficient information available, so that all parameters are estimable. This is a problem when the available indices are of the biomass type. In most assessment problems, the availability of a biomass index (e.g. catch weight per unit effort) will not be sufficient to allow full estimation of the state of the stock. In this section, the "tuning series" are presented as a CPUE series obtained by research vessels (e.g. a bottom trawl survey). It is assumed that this survey will provide a valid index for all age groups and that all data have the same error distribution. It is however not assumed that the sampling efficiency (the catchability) is the same for all age groups. This assumption of fixed error is relaxed in Section 8.3 where relative weighting of the data series is discussed.

This procedure was presented by Gavaris (1988). Stefansson (1997) gives a practical guide to the method.

## 8.1 ADAPT WITH EXTERNAL WEIGHTING

The ADAPT framework assumes that all deviations between the model and the observations are due to measurement error. It does not make any explicit assumptions of the error structure, but assumes that the least-squares estimator is applicable. The distribution of measurement errors in biological investigations is often not symmetrical, and therefore it is customary to work on logarithmic values. This has been found to be more appropriate in most real stock assessments.

The estimation is to find the minimum of the least-squares sum. This sum now has at least two terms, the catch and CPUE:

$$\sum_{a\in age}\sum_{y\in year}\left[\ln Catch_{ay}^{obs}-\ln Catch_{ay}^{\mathrm{mod}}\right]^2+ \sum_{a\in age}\sum_{y\in year}\left[\ln CPUE_{ay}^{obs}-\ln CPUE_{ay}^{\mathrm{mod}}\right]^2=MIN\{\text{model parameters}\} \tag{86}$$

The sum range over age and year may not be the same for the catch and the CPUE data. For the catch, the model in numbers by age and by year is:

$$\ln Catch_{ay}^{\mathrm{mod}}=\ln P_{ay}+\ln F_{ay}+\ln\left(\frac{1-\exp(-Z_{ay})}{Z_{ay}}\right)$$

with (87)

$$Z_{ay}=F_{ay}+M_a$$

and for the CPUE data the model is:

$$\ln Cpue_{ay}^{\mathrm{mod}} = \ln q_a + \ln \tilde{P}_{ay}$$

with

$$\ln \tilde{P}_{ay} = \ln P_{ay} - \alpha Z_{ay} + \ln\left(\frac{1-\exp(-(\beta-\alpha)Z_{ay})}{(\beta-\alpha)Z_{ay}}\right) \tag{88}$$

and

$$Z_{ay} = F_{ay} + M_a$$

The parameters are the matrices: population in number $P_{ay}$ or the fishing mortality $F_{ay}$. The natural mortality $M_a$ and the parameters $\alpha$ and $\beta$ relating the timing of the survey to the stock calculation are provided as external parameters. $\alpha$ and $\beta$ are the start and end point in time of the observation given as a fraction of the year.

The problem can be reduced by assuming that the noise in the catch data is much less than the errors in the CPUE data and therefore the catch term in the sum of squares can be fulfilled exactly. This means that all fishing mortalities and all population sizes can be written as a function of the fishing mortality in the terminal year for all age groups and of the terminal age for all years. This reduces the parameters to the log catchabilities and the terminal log fishing mortality (or equivalently the terminal log population of survivors). A further reduction is to note that the least-squares estimator for the log catchabilities can be found explicitly as:

$$\ln q_a = \frac{\sum_y \left(\ln CPUE_{ay}^{obs} - \ln \tilde{P}_{ay}\right)}{n} \tag{89}$$

where $n$ is the number of years in the sum. After these reductions, the problem is to find the minimum of the sum-of-squares:

$$\sum_{a\in age}\sum_{y\in year}\left[\ln CPUE_{ay}^{obs} - \ln\left(\frac{\sum_y \left(\ln CPUE_{ay}^{obs} - \ln \tilde{P}_{ay}\right)}{n}\right) - \ln \tilde{P}_{ay}\right]^2 = MIN\{\text{Terminal } F's\} \tag{90}$$

The algorithm to find these unknown parameters consists of the following steps:

(i) Initiate the unknown parameters, $\ln(F)$ or $\ln(P)$, with guessed estimates.

(ii) Perform a VPA to estimate population and fishing mortality coefficients for all age groups and years.

(iii) Calculate the $\ln(q_a)$ parameters.

(iv) Calculate the sum-of-squares using the VPA solution and the calculated log catchabilities.

Steps (ii)-(iv) need to be imbedded in an iterative routine to find the minimum of the sum-of-squares.

The results are:

- Estimates of the abundance $P_{ay}$.
- Estimates of fishing mortality coefficients $F_{ay}$.
- Diagnostic information. This includes residuals calculated for the CPUE index and the standard errors of parameters, terminal fishing mortalities or terminal survivors, the coefficients of variation of these parameters, the correlation matrix of the parameters (Chapter 7).

The ADAPT procedure works best when catches are the dominating cause of mortality (i.e. $F > M$). This is the case for many important fish stocks (e.g. Halliday and Pinhorn 1996, Serchuk *et al.* 1996). With the introduction of the precautionary approach, hopefully there will be increasing numbers of examples where $F >> M$ no longer applies. The estimation procedures are then more prone to noise in the abundance index data than if $F > M$. In practice, this is illustrated by the instability in the estimated stock sizes that occur in the assessments between two neighbouring years.

The ADAPT estimates are functions of the natural mortality coefficient. From VPA, it is known that the estimated $F + M$ is fairly constant locally around the chosen value of $M$. The VPA behaviour dominates the ADAPT calculations except for the most recent years where the results are very dependent on the input values for the oldest age and for the terminal year in the assessment. Even so, for the most recent year the fishing mortality estimate will still be lower with larger natural mortality values.

## 8.2 SEVERAL ABUNDANCE INDICES

Normally several abundance indices are available and the object function is expanded to include these:

$$\begin{aligned} Lsq = & \sum \left( \ln Catch^{obs} - \ln Catch^{teo}(F,N) \right)^2 \\ & + \sum \left( \frac{\ln Cpue_1^{obs} - \ln Cpue_1^{teo}(F,N,q_1)}{\sigma_1} \right)^2 \\ & + \sum \left( \frac{\ln Cpue_2^{obs} - \ln Cpue_2^{teo}(F,N,q_2)}{\sigma_2} \right)^2 \end{aligned} \qquad (91)$$

The weights that are required are the variances ($\sigma^2$) of the CPUE indices. These should be readily available from the surveys. In the formulation above these weights are expressed relative to the accuracy of the catch data, a problem that is often less tractable than the estimation of the variance from the surveys. This is because of the way the catch-at-age matrix is built from many different sources and in some cases

there is no direct age-length key available for a portion of the total catch. In these cases one of the available ALKs is used which is thought to best represent that catch, but it is difficult to assess the variance and bias that such a procedure may produce in the catch-at-age matrix. In practice, the problem is unresolved and the CPUE indices (or other stock indicators) are given equal weight, while the catches are assumed to be estimated with far less variance than the surveys and hence this contribution is given infinite weight, i.e. the catch equation is fitted exactly.

## 8.3 EXTENDED SURVIVOR ANALYSIS (XSA)

This is the standard procedure used in ICES (Darby and Flatman 1994, Shepherd 1999). The method is different from the approach presented above in that the procedure does not define an object function. Instead, XSA is based on an iteration procedure of the functional type. The method is of the same type as the ADAPT presented above, the data are catch-at-age in numbers by age and by year supplemented by stock abundance indices. However, the approach is restricted as only age dis-aggregated abundance indices can be used.

The basis of the method is the link between the population and the abundance index through the catchability $q$:

$$Cpue = qN^{\gamma} \tag{92}$$

where $q$, $\gamma$ vary with abundance index and with age, but is constant with respect to time. The CPUE values are all corrected to refer to the stock at the beginning of the year using the usual formula:

$$Cpue_{ayf} = Cpue_{ayf}^{obs} / \left[ \exp(-\alpha(F_{a,y} + M_a)) \frac{1-\exp(-(\beta-\alpha)(F_{ay}+M_a))}{F_{ay}+M_a} \right] \tag{93}$$

where $\alpha$ and $\beta$ are the start and end point in time of the observation given as a fraction of the year.

The XSA iteration starts with an initial guess of the number of survivors (population at the end of the year of the oldest age group included in the analysis) and $M$. The XSA then applies a standard VPA to the catch-at-age and year data to provide stock sizes $N$. Based on these stock sizes the catchability $q$ and the exponent $\gamma$ can be estimated by linear regression (Equation 67):

$$\ln N_{ay}^{VPA} = \frac{1}{\gamma_{af}} \ln Cpue_{ayf} - \frac{\ln q_{af}}{\gamma_{af}} \tag{94}$$

where the subscripts $a$ = age, $y$ = year and $f$ = fleet. The regression is hence over years for fixed age and fleet.

When the catchability and the exponent in the CPUE–stock relation has been determined, the next step is to correct the stock estimate by:

$$\ln N_{ayf}^{corr} = \frac{\ln Cpue_{ayf} - \ln q_{af}}{\gamma_{ay}} \quad (95)$$

so that each abundance index estimates the stock in numbers by age and by year. These estimates are then averaged to provide a new starting point for a new VPA. This average is based on calculating the number of survivors of the oldest age group included in the catch-at-age analysis

$$\ln N^{survivors} = \ln\left[\frac{Cpue_a}{q_a}\right] - F_{a,cum} - M_{a,cum} \quad (96)$$

where the fishing mortality $F$ and natural $M$ are cumulative over age ($a$) until the oldest age included in the analysis. For a given cohort, there will be a number of such estimates of survivors. These come from different age groups observed in the same abundance index and from different indices (e.g. commercial CPUE and research vessel surveys). The XSA combines these weighted estimates into a single estimate of the survivors of that cohort. This estimate is then introduced into a VPA of the catch in numbers by age and by year thereby obtaining stock in numbers and fishing mortality. This concludes the iteration loop. The next iteration loop begins by using these estimates to calculate the catchabilities ($q_a$) by age and by index type. The whole process is repeated until convergence. However, convergence is not guaranteed and there are examples where the iteration diverges.

The weights used for the survivor estimates are the inverse prediction variance around the regression carried out to estimate the catchabilities, multiplied by $F_{a,cum}$.

## 8.4 DOWN WEIGHTING OF OLDER DATA IN THE ANALYSIS

The segments of the time series may be of a different relevance. Fisheries develop and therefore catchabilities estimated from data that stretch far back in time may be of little use for an assessment that focuses on projecting the future. It therefore appears reasonable to introduce a down-weighting of older data. This can be done by simply restricting the analysis to the most recent 10-15 years of data or a more gradual down weighting with a time taper. In a common implementation of XSA, explicit weighting of the residuals with the year is introduced as a time taper (Darby and Flatman 1994).

$$W_{year} = \left[1 - \left(\frac{\text{Taper range - year}}{\text{Taper range}}\right)^p\right]^p \quad (97)$$

for year = 0,...,Taper range.

The taper range in the Lowestoft package is set at a default value of 20 years, so only the last 20 years catch or CPUE are included in fitting the model. The default taper is a tricubic type (p=3). The introduction of such a time taper modifies the object function to:

$$\sum_{a\in age}\sum_{y\in year} W_{year}\left[\ln Catch_{ay}^{obs} - \ln Catch_{ay}^{\mathrm{mod}}\right]^2 + \sum_{a\in age}\sum_{y\in year} W_{year}\left[\ln CPUE_{ay}^{obs} - \ln CPUE_{a,y}^{\mathrm{mod}}\right]^2 = MIN\{\text{model parameters}\} \quad (98)$$

## 8.5 REGULARISATION

The basic idea of regularisation is to assume that the exploitation pattern and the fishing mortality do not change abruptly from one year to the next. The estimation equation is therefore expanded, but includes a penalty for changes in fishing mortality. These methods include the shrinkage implemented in the XSA version of the Lowestoft/ICES software.

In many fisheries assessment problems, it is reasonable to assume that certain variables vary slowly (e.g. the fishing mortality). The basis for such assumptions is that an effort increase may require additional fleet capacity to be built that takes 1-2 years. The technical formulation of this assumption is to add an extra term to the least-squares equation. This means that the final least-squares expression to be minimised becomes:

$$\sum_{ay}\left(\ln C_{ay}^{obs} - \ln C_{ay}^{teo}\right)^2 + \sigma\sum_{ay}\left(\ln Cpue_{ay}^{obs} - \ln Cpue_{ay}^{teo}\right)^2 + .... + \lambda\sum_{ay}\left(\ln F_{a,y+1} - \ln F_{ay}\right)^2 = MIN \quad (99)$$

The regularisation parameter ($\lambda$) controls how much variation between years is expected in the fishing mortality. The parameter should be supplied by the user and is given in units of inverse variance relative to the weight applied to the catch-at-age data. The example of the regularisation above is given in logarithmic terms, but this term can also be arithmetical.

Making estimates conditional on past values may not only represent the behaviour of the fishery more closely, but also improve the statistical behaviour of the fit. This can be seen more clearly by considering how the estimates change as $\lambda$ in Equation 99 increases. As $\lambda$ gets larger, there is an increasing "cost" to differences between sequential $F$'s, so as $\lambda$ approaches infinity Equation 99 can only be minimised by making $F_{ay} = F_{a,y+1}$, so all $F_{ay}$'s are equal for all $y$. In essence, we would only be estimating one parameter, a best-fit $F_a$. Conversely, as $\lambda$ approaches zero, we return to estimating an independent fishing mortality for each age in each year. As $\lambda$ takes on values between these two extremes, the effective number of parameters being estimated varies continuously. In general, the fewer parameters there are (higher weight $\lambda$), the more reliable the estimates, but the poorer the model fits the data. This, and similar time series techniques, can allow a stock assessment to balance improving the model fit against estimate reliability.

Shrinkage as introduced in the XSA package belongs to this class of regularisation. In that implementation, the fishing mortalities after the estimation are regressed on a moving average:

$$F_{ay} = (1-\theta)\tilde{F}_{ay} + \theta \frac{\sum_{j=1}^{J} F_{a,y-j}}{J} \tag{100}$$

where $J$ is the number of years used to calculate the moving average, $\tilde{F}_{ay}$ is the proper estimate from the minimisation algorithm and $\theta$ is a weight parameter ($0<\theta<1$) controlling how much weight should be given to the "shrinkage". The population estimate of the last year can be treated similarly.

# 9 ASSESSMENT RESULTS

## 9.1 PROJECTIONS OF FUTURE YIELDS AND STOCK DEVELOPMENT

Projection of future yields under specified fishing scenarios is one of the two essential elements in fishery management advice based on fish stock assessment. The other is evaluation of these scenarios relative to a desired stock status defined through the reference points. Projections are done using the Thompson and Bell procedure described in Sparre and Venema (1998). The presentation given in this manual extends this procedure to include an account of the uncertainty in the following factors:

- Knowledge of the stock at the outset of the projection, which depends on:
  - the reliability of the catch data,
  - the amount of sampling of these catches, possible bias in sampling and in age reading,
  - the availability, accuracy and precision of the abundance indicators, e.g. CPUE from research surveys,
  - understanding the relation between the abundance indicators and the stock.
- Future population dynamics (i.e. recruitment, growth, maturity, fecundity, etc.), which depends on:
  - the recruitment estimates, which can be obtained from pre-recruit surveys, a stock-recruitment relationship or from environmental conditions depending on the biology,
  - the mean weight per individual in the catches and in the stock (either total stock or in the spawning stock only),
  - the future maturity ogive and fecundity,
  - natural mortality.
- Translation of the specified fisheries policy into fishing mortality and the stock available to the fishery, which depends on:
  - the accuracy of the specified relationship between fishing mortality and effort,
  - knowledge of stock distribution in space and time by age groups,
  - knowledge of the fleet reaction to changes in stock sizes, alternative fishing opportunities, regulations, etc.

Dependent on the specific stock under investigation, the projection procedure will often be restricted to include only the uncertainty in the initial stock estimate and in the prediction of future recruitment through the stock-recruitment relation (ICES 1995a, 1997 and 1998). Projections based on multispecies VPA also include variation, but not uncertainty in the natural mortality. In particular, translating fisheries policy into fishing mortality is often dealt with rather unsystematically.

The stock size can be projected using the procedures above to calculate the stock of survivors, that is the initial stock composition at the start of the period of projections. However, this is not sufficient for the purpose of providing fishery management advice. Management requires projection of the yield (in weight) and of stock indicators, most often recruitment trends and spawning stock biomass (SSB). To estimate the latter it is necessary to estimate mean weights per individual for the catches, the stock and spawning stock. When calculating the spawning stock the maturity ogive is also required. Ideally, this model should be expanded to include additional elements like the sex ratio and the fecundity, but this is seldom done. The mean weight-at-age and the maturity ogive used in projections are usually based on simple time series regressions. Often a mean of the last three years is used.

Biomass-based reference points are nearly always based on SSB, which is one of the most important stock status indicators. SSB is calculated based on stock in numbers, a maturity ogive and mean weights per individual by age. Many of these parameters vary between years. Therefore, among other checks, whether an overall maturity ogive is applicable or whether this ogive needs to be established for each spawning season should be investigated for each individual stock. There may well be other parameters that are also relevant for the calculation of the SSB, such as a year class-dependent female to male ratio, or age-dependent fecundity and hatching success (Rijndorp 1993).

When providing management advice the fishing scenarios should be evaluated in the light of the projected stock status in the short, medium and long term. The desired stock status is specified based on "biological reference points" (Caddy and Mahon 1995). The calculation of some of these reference points and some extensions is discussed in Section 9.5.1.

Fisheries management however, does not formulate the regulations in biological reference points, but in management tasks, such as an annual TAC, closed area or effort limitation. We therefore need tools that allow translation of the reference points projection into the management activities. Since management is based on socio-economic and political considerations, decisions are often not direct translations of the biological advice. Therefore, it is necessary to calculate the fishing mortality and exploitation pattern that will result from any decision made by management, so that management can see the biological implications.

We distinguish between short-term, medium-term and long-term projections according to the degree of dependence on the current stock status (Figure 9.1).

- **Short-term projections:** the time period in which the estimated stock composition of the terminal year still dominates future yields. For example, more than 50 % of the yield is from cohorts in the terminal year. This short-term time period is often only 2-3 years.

- **Medium-term projections:** the time period in which the estimated stock composition of the terminal year still has some influence on future yields. For example, more than 10% of the yield is from cohorts in the terminal year. The medium term time period is often 5-10 years.

- **Long-term projections:** the projected equilibrium state, usually including stochastic variation from recruitment and population dynamic parameters.

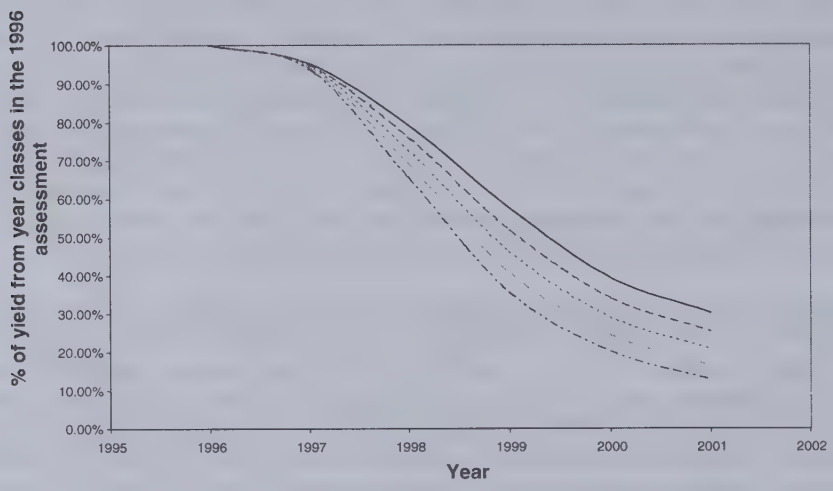


**Figure 9.1 Percent of projected yield (Baltic cod ICES subdivisions 25-32) from year classes estimated in the 1996 assessment for 5 exploitation levels. As the projection is extrapolated into the future, the dependence of yield on the current assessment falls.**

Interpretation of the projections varies substantially between time horizons. Short-term projections are used for calculating the TAC in subsequent years; medium-term projections are used for discussion of the consequences of the policy on which the TAC in a specific year is established. Finally, long-term equilibrium projections are used as background for this discussion, in particularly for measuring the policy relative to the biological reference points.

TACs are often used for regulating fisheries in the North Atlantic (see overview Halliday and Pinhorn 1996). This management measure establishes an overall limit on the total amount than can be removed from the stock, most often measured in weight but for large fish the removal limit may also be established in number of fish (e.g. Baltic salmon). This application often involves a 2-year projection, the year in which the assessment is made and the subsequent TAC year.

## 9.2 SHORT TERM PROJECTIONS

Short-term projections are usually made by the Thompson and Bell procedure (Sparre and Venema 1998, Section 8.6). The procedure projects the estimated age

composition of the terminal year into the near future. This near future is the time period in which the estimated stock composition of the terminal year still dominates future yields, e.g. more than 50% of the yield is from year classes appearing in the estimated stock composition for the terminal year.

The mean weight-at-age and maturity ogive are often taken as the mean of the most recent three years or a similar simple method. The link between the calculated yield in the year of projection and the fishing mortality is usually established through the separable fishing mortality model. The projection assumes that the selectivity pattern ($S_a$) for the most recent years also applies in the near future and it is effort ($E_y$) that is adjusted. Sparre and Venema (1998) reformulate the Thompson and Bell model as $F_{ay} = X\, E_{most\ recent\ year}\, S_a$ , and it is the factor $X$ ($X$ = 1 for the recent level of fishing mortality) that is used to adjust the projected exploitation rate in the analysis. This procedure makes the determination of the exploitation pattern, also called the partial recruitment, an important issue (e.g. Rivard 1983).

If we have applied an estimation method based on separable VPA (e.g. ICA or CAGEAN) then the exploitation pattern ($S_a$) is estimated directly. If some other method was found more appropriate for the estimation of the stock status, then for the projections a model of how the fishing mortality by age will vary with stock size and other parameters is required. For this, the separable VPA model is often used. The calculation of the exploitation pattern based on the separable VPA model is as follows.

Assuming that the estimation procedure provided $F_{ay}$ and that the error is log-normally distributed, then the exploitation pattern is calculated as:

$$\ln S_a = \frac{\sum_y \left(\ln F_{ay} - \ln E_y\right)}{n} \qquad (101)$$

where n is the number of years that is summed over. To avoid estimating a redundant parameter in the multiplicative separable VPA model, $S_a$ is normalised by setting $S_{a'} = 1$ for some $a'$ and therefore:

$$\ln S'_a = \frac{\sum_y \left(\ln S_{ay} - \ln S_{a'y}\right)}{n} \qquad (102)$$

For example, Rivard (1983) normalised each *F-at-age* array with the maximum element value for that year, then averaged the normalised values across years, and finally applied yet another normalisation with the maximum value in this averaged array.

Another approach would be to use a linear model and find the parameter array $S_a$ using a generalised linear model (McCullagh and Nelder 1983). Note that the solution, if the log-normal is assumed, will give the same result as Equation 101, but other models can be tried. In particular, there is little reason not to include the separable model as a link model in the VPA analysis (Equation 42) if an independent measure of the overall exploitation rate (i.e. effort) is available.

## 9.3 STOCK RECRUITMENT

Projections are based on estimates of stock productivity. The standard short-term projection accounts for growth and mortality, while the recruitment is not dealt with in depth. To be able to extend projections beyond the short term requires that more emphasis be placed on the model of recruitment.

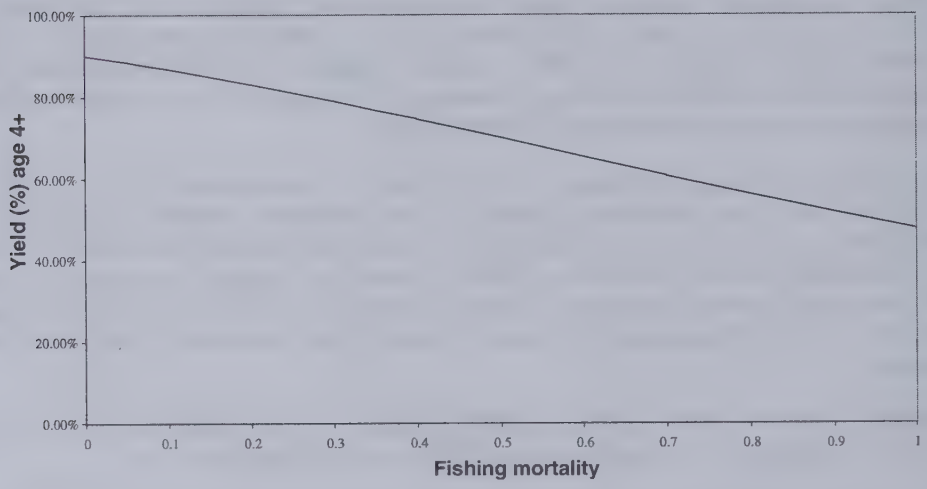


**Figure 9.2 Equilibrium yield of age 4+ as a percentage of total equilibrium yield in Baltic cod ICES subdivisions 25-32 based on the average exploitation pattern for years 1992-1996.**

Applying a simple (often geometric) mean recruitment may be a reasonable procedure in short-term projection where the mean recruitment over recent years may be appropriate as the best guess of the strength of future recruitment. A fixed mean or time trend regression of recruitment may be adequate because the projection of the different fishing options is insensitive to the recruitment assumption. Where projections result in quite different levels of spawning stock biomass (SSB), a stock recruitment relationship may improve the accuracy of the forecast. The stock recruitment relation is also required for many of the reference points discussed in Section 9.4 as these attempt to account for stock productivity under heavy exploitation and therefore at low SSBs.

Traditionally there are two different S-R models in fish stock assessment: the Beverton and Holt (B&H, Beverton and Holt 1957) and Ricker models (Ricker 1954). Both these models have two parameters, but can be generalised into a single three parameter model of which these two are special cases (Deriso 1980, Schnute 1985). There are other models which have been proposed (e.g. Shepherd 1983, Patterson 1998a), but the likely forms of the S-R relations are well covered by the general Deriso-Schnute model, and most often the B&H and Ricker models suffice.

The B&H relation is similar to the logistic model. It has a carrying capacity, here the asymptotic maximum recruitment ($\alpha$) obtained from the spawning stock biomass ($SSB$).

$$R = \frac{\alpha}{1 + \beta / SSB} \tag{103}$$

The parameter $\beta$ is the spawning stock biomass where the recruitment ($R$) is half of its potential maximum. The biological concept behind the model is that the egg production – assumed proportional to the SSB – approaches a limit, which is set by a density-dependent mechanism. Density-dependent mortality increases natural mortality in the egg, larvae and early fish life phases, so that the absolute number of survivors remains effectively constant at larger SSB levels. Where the asymptote is reached at a small SSB, the recruitment will appear constant except in cases of severe overfishing.

The Ricker stock recruitment curve is based on a feedback mechanism. For spawning stock biomass above some optimum the mortality in the egg, larvae and early fish life phases increases at such a rate, that this leads to a decrease in the recruitment. This feedback could be the result of cannibalism where the adult population has a negative impact on the survival success of its offspring.

The relation is:

$$R = \alpha \, SSB \, e^{-SSB/K} \tag{104}$$

The first parameter $\alpha$ controls the slope at origin and as we shall see this is important for the limit and target reference points. The parameter $K$ is the SSB when the recruitment is at its maximum.

The Deriso-Schnute generalisation has three parameters:

$$R = \alpha_0 (SSB/K)\left(1 - \gamma (SSB/K)\right)^{1/\gamma} \tag{105}$$

| **Model** | $\gamma$ | **Formula** |
|---|---|---|
| Proportional | $-\infty$ | $R = \alpha_0 \, SSB/K$ |
| Beverton and Holt | -1 | $R = \dfrac{\alpha_0}{1 + (K/SSB)}$ |
| Ricker | 0 | $R = \alpha_0 \, (SSB/K) \, e^{-SSB/K}$ |
| Quadratic | 1 | $R = \alpha_0 \, (SSB/K)(1 - SSB/K)$<br>SSB < K |

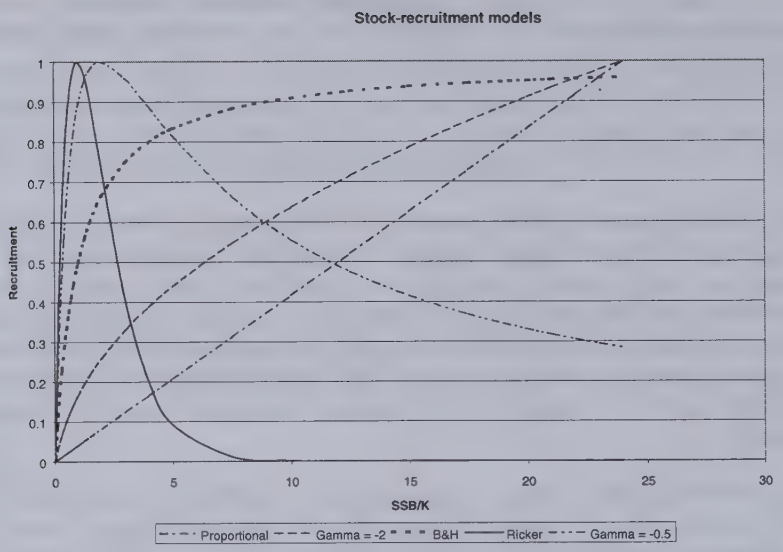


**Figure 9.3 The main stock recruitment relations as described by the main models. The alternative models can be produced for different parameter values ($\gamma$) of the Deriso-Schnute model.**

where the form of the relationship is controlled by the $\gamma$ parameter as follows (see Table above and Figure 9.3).

In fish stock assessment, recruitment is often measured at the age when the stock recruits to the fishery rather than when the larvae hatch. The life history between the egg stage and when the fish appears in the fishery is often not well documented. However, it is expected that life history parameters in the early life stages (e.g. the natural mortality) are different than later in the life cycle. The S-R relation usually takes into account the survival from egg until the fish recruits to the fishery.

### 9.3.1 Fitting the Stock-Recruitment Curve

The estimation of the stock-recruitment curve is based on a standard least-squares fit. A common problem is that the stock recruitment curve fits the data poorly and there are significant outliers, where the predicted recruitment based on SSB is very far from the actual year class strength. Analysis of the influence of outliers on the estimated parameters is therefore a prominent part of this analysis.

There are two approaches to the problem.

1) The VPA estimation procedure may be used to estimate recruitment and spawning stock biomass and then the stock-recruitment curve is fitted to these estimates or

2) The stock-recruitment relation may be included directly in the estimation procedure.

The latter approach would mean that the population size (stock in numbers) at the recruitment age would be based upon the stock recruitment relationship, so the least-squares estimation procedure could be to minimise the following function:

$$\sum_{y}\left(\ln C_{0y}^{obs}-\left[\ln \tilde{N}_{0y}+\ln\left(F_{0y}\frac{1-\exp(-Z_{0y})}{Z_{0y}}\right)\right]\right)^2 + \sum_{a>0,y}\left(\ln C_{ay}^{obs}-\ln C_{ay}^{teo}\right)^2+\sum_{a,y}\left(\ln Cpue_{ay}^{obs}-\ln Cpue_{ay}^{teo}\right)^2+\ldots = MIN \quad (106)$$

where

$$\ln N_{0,y}=\ln\frac{A}{1+B/SSB_y}$$

$$\ln Cpue_{ay}^{teo}=\ln q_a+\ln \tilde{N}_{ay} \quad (107)$$

$$\ln C_{ay}^{teo}=\ln N_{ay}+\ln\left(F_{ay}\frac{1-\exp(-Z_{ay})}{Z_{ay}}\right)$$

where the $\tilde{N}$ is the population size relevant for the abundance estimate, corrected for timing of the survey or averaged over the relevant period of the year.

It is usually advisable to introduce a transformation, such as a logarithms of both the recruitment and the spawning stock biomass, because of highly skewed variation usually seen in these types of data. Alternatively, the S-R model could be fitted using robust regression (Section 6.5).

## 9.4 MEDIUM-TERM PROJECTIONS

Short-term projections focus on the development of the existing population in the year of the assessment. This may be misleading as the fishing mortality could be in a region where the stock is overexploited, but the most recent year classes by chance are strong. Therefore, short-term prediction is supplemented with medium-term prediction to illustrate the stock development and in particular to investigate if the stock is expected to increase or decrease if normal recruitment prevails.

Medium-term analysis also includes the uncertainties in the stock status and in the projections. These uncertainties include the variance of the estimates from the assessment of the state of the stock, from the uncertainties on what fishing mortality the management measures will produce and from the future population dynamics (e.g. recruitment, mean weights, maturity ogive and natural mortality). Several of these uncertainties may be correlated (e.g. high stock abundance may be correlated with slow growth) and a simple sum of all these uncertainties may therefore overestimate the true variance on the projections.

The projected yield and stock are therefore subject to uncertainties that originate from:

- The initial stock size.
- Future recruitment.
- Population dynamic parameters and variables, e.g. mean weight-at-age, natural mortality, etc.
- The fishing mortality in the years of projection. Fishing mortality may be controlled by management measures, e.g. from a TAC.

It is standard practice to only include separate errors from the initial stock size and stock-recruitment in projections. Errors due to changes in population dynamics parameters and management measures are usually ignored. This concentrates on sources of uncertainty, which should have greatest impact on management controls. In this form, it is also easier to study the link between the management controls (e.g. effort) and fishing mortality.

These error contributions have different statistical properties. The initial stock size may have log-normal distributed observation errors, while the recruitment process is often considered as a stochastic process with log-normal variation. The management implementation errors (i.e. that the fishing mortality intended is not realised) are usually ignored. The system is often investigated using Monte Carlo simulation rather than attempting a full analytical solution to the problem.

### 9.4.1 Projection Methods

Medium-term projections are stochastic simulations where, in particular, the variation in the recruitment is included in the analysis. It is quite possible, and in some cases desirable, to include the variability of other biological parameters in the projections. The result is a time diagram showing curves, for example, of the 5, 25, 50, 75 and 95 percentiles of the projection of the relevant stock indicators such as spawning stock biomass, yield and recruitment. The projections are usually made for well-defined fishing scenarios, for example with a harvest control law. Typically, the control is very simple, such as a constant fishing mortality throughout the entire period.

The noise in recruitment can be derived from any of three different procedures:

- **Direct bootstrapping of recruitment without any particular biological stock recruitment model:**. This assumes past recruitment random distribution will be the same as future recruitment and requires a long time series.
- **Empirical bootstrap:** Estimation of the S-R relation and bootstrapping of the residuals. This also requires a long time series, so bootstraps can be drawn from a reasonable sample of residuals.
- **Parametric bootstrap:** Estimation of an S-R relation and fitting the residuals to some statistical model of the random noise (e.g. log-normal). Then simulate recruitment from the S-R relation with an added noise term taken from a random number generator. This is preferred if the number of residuals is small.

## 9.5 LONG-TERM CONSIDERATIONS

Long-term projections consider the general state of the stock in relation to reference points. These ignore short-term fluctuations, but consider the long-term status under different exploitation rates. They are used to indicate the direction management controls should take to improve the status of the stock.

Biological reference points are discussed in detail in Caddy and Mahon (1995). Reference points are introduced here to provide a method to assess the general exploitation level of the stock. The biological reference points only consider the state of the stock, so there is no consideration of the economics or the social well-being of the fisheries.

Reference points fall into two groups:

- Limit reference points. These points are upper limits on the exploitation that should not be approached.

- Target reference points. These are levels of exploitation that should be targets for fisheries management.

In terms of fisheries management the limit reference points define the "space" within which the manager should maintain the stock. The reference points are biological states that help in an evaluation of the stock. Because of the uncertainties involved in all steps of the management procedure, it is usually advisable that management objectives include a buffer to the limit reference points to ensure that the stock remains healthy.

Stocks are said to be within safe biological limits when there is a high probability that

1) The spawning stock biomass is above the threshold where recruitment is impaired, and

2) The fishing mortality is below that which will drive the spawning stock to the biomass threshold.

The biomass threshold is defined as $B_{lim}$ (subscript $lim$ stands for limit) and the fishing mortality threshold as $F_{lim}$. The accuracy with which the thresholds and current status of the stocks are known, and the risk that is tolerable, are important factors in determining the distance away from the threshold that can be accepted. The greater the accuracy of the assessment, the smaller the distance between the limit and precautionary reference points that would define the target. If the assessment is less reliable, the distance needs to be greater. Within ICES, $B_{pa}$ (subscript $pa$ stands for precautionary approach) is defined as the biomass below, and $F_{pa}$ as the fishing mortality above which management action should be taken. The distance between the limit and the precautionary approach reference points is also related to the degree of risk that fishery management agencies are willing to accept.

Formal definitions are provided below:

- $F_{lim}$ is the fishing mortality limit that should be avoided with high probability because it is associated with unknown population dynamics or stock collapse. $F_{lim}$ is usually set so that the spawning stock biomass will remain above a threshold below which the probability of good to average recruitment is too low. There are very few stocks for which $F_{lim}$ is accurately known. Some stocks in the ICES area have collapsed in the past when fishing mortality exceeded $F_{lim}$. Generally there are great uncertainties in the estimate of $F_{lim}$, as well as the estimates of current fishing mortality.

- $F_{pa}$ is the fishing mortality that should be the target for management of the stock under the precautionary approach. In order to have a high probability that fishing mortality will be below $F_{lim}$, a precautionary reference point, $F_{pa}$ is defined. Used as a constraint on fishing, $F_{pa}$ is designed to ensure that there is a high probability that fishing mortalities greater than $F_{lim}$ will be avoided. It is the upper bound on fishing mortality rate to be used by ICES in providing advice. $F_{pa}$, should be set in the range of previous fishing mortalities, and maintain a biomass within those perceived to be acceptable.

- $B_{lim}$ is the limit spawning stock biomass, below which recruitment is impaired or the dynamics of the stock are unknown. Stocks may become depleted due to reduced recruitment even if fishing mortality is successfully maintained at or below $F_{pa}$. Furthermore, restraining fishing below $F_{pa}$ may not be successful and biomass may decline as a result. Clearly, therefore, in addition to a constraint on fishing mortality, it is desirable to have a biomass-based constraint to prevent stock decline to values where expected recruitment is low or unknown. Whereas $F_{pa}$ defines an "overfishing threshold", a definition of when the stock is regarded as being in a "depleted state" is also necessary.

- $B_{pa}$ is defined to ensure a high probability of avoiding reducing the stock to a point, $B_{lim}$. $B_{pa}$ is the biomass below which the stock would be regarded as potentially depleted or overfished. When SSB is below $B_{pa}$, fishing mortality may need to be reduced below $F_{pa}$ to allow recovery.

### 9.5.1 Biological reference points

To establish the value of $F_{pa}$ and $B_{pa}$, a number of other reference points can be used. The list given below is not exhaustive, but includes some of those most often used.

#### *9.5.1.1 Reference points defined on optimal yield considerations*

The traditional target is $F_{max}$ (Beverton and Holt 1957). This is the maximum on the yield-per-recruit curve and as such does not take into account the effect fishing may have on recruitment. Therefore, $F_{max}$ is a long-term reference point only if recruitment is independent of the spawning stock biomass over applicable ranges of fishing mortality. Another reference point often derived from the yield-per-recruit curve is $F_{0.1}$, the fishing mortality where the slope on the yield-per-recruit curve is 10% of the slope at the origin. This is more conservative, and results in little overall loss in yield with the benefit of a relatively large decrease in fishing mortality.

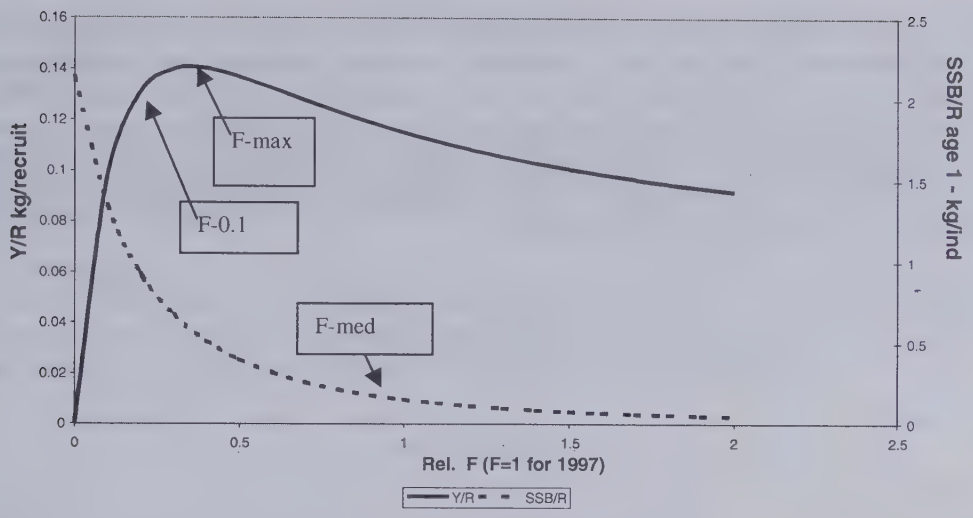


**Figure 9.4 Yield-per-recruit for Peruvian hake under different target reference points.**

The extension of $F_{max}$ to include a stock recruitment relation produces a new reference point, $F_{MSY}$. This is done by applying the equation Yield = Recruitment · (Yield/Recruit) and finding $F_{MSY}$, which is the fishing mortality where the yield is at its maximum. In order to establish the equilibrium recruitment level, we need the equilibrium spawning stock biomass (SSB), which is obtained by solving the non-linear yield and population equations.

Another reference point is where $SSB_{eq} = 0$ (subscript $eq$ implies an equilibrium solution), also called $F_{crash}$ (Cook *et al.* 1997). This is the minimum fishing mortality where the stock will go extinct.

Any of the stock recruitment relations (Section 9.3) can be used with the Thompson and Bell yield calculation. For each value of $F$, the equations can be solved to find the equilibrium recruitment from the stock-recruitment relation and the derived SSB. Then the yield is calculated. Although the models may be complex and non-linear, these are essentially one dimensional problems (solve for $F$ or $SSB$), and so solutions can be found using simple methods such as bisection.

### *9.5.1.2 Reference points designed to ensure reproductive capacity of the stock*

These reference points focus on the stock recruitment relationship. The basic idea is to make sure that the spawning stock biomass is sufficient to guarantee the full reproductive capacity of the stock. Therefore, it is assumed that the relation between the stock and recruitment has some SSB beyond which recruitment is independent of the SSB. This point is often called Minimum Biological Acceptable Level (MBAL). The B&H type stock-recruitment curve shows such behaviour with an asymptotic recruitment level independent of the SSB for large SSB values. For the Ricker curve,

where a larger SSB leads to decreasing recruitment, the analysis is confined to the right hand part of the curve.

MBAL does not have a strictly formal definition, but it is the point where the stock-recruitment curve begins to show a positive correlation between the spawning stock biomass and the recruitment, hence the point where the recruitment is impaired by reduced SSB. The MBAL is often related to the Beverton and Holt curve, and as such may be defined using the B&H $\beta$ parameter (Equation 103, Figure 9.5), which defines the point where the recruitment is half the asymptotic maximum. MBAL is in many applications used as a $B_{lim}$ reference point.

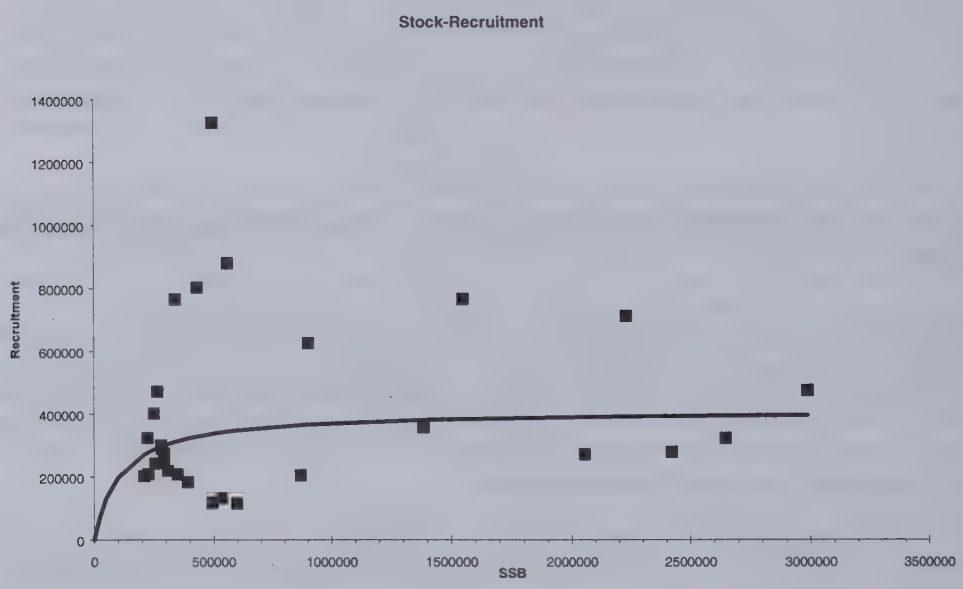


**Figure 9.5 An example fitted B&H stock recruitment relationship, where $\beta$ = 106 871 t. This suggests that an MBAL would be around 110 000 t or possibly a little higher. Inspection of the graph suggests that the recruitment is very variable, but also that, on average, recruitment has not been impaired at the SSB levels observed.**

### *9.5.1.3 Reference point defined based on historic performance of SSB/R*

A reference point of this class based on fishing mortality is the $F_{med}$ and the associated $F_{low}$ and $F_{high}$. These reference points are defined based on the historic performance of the recruitment of the stock. Therefore, they are only relevant as a possible basis for precautionary reference points if the stock is in good "health".

The formal definition of these reference points is

$$
\begin{aligned}
&Median(SSB_y / R_y, y = 1,2,...) = (SSB / R)_{eq} \quad for\ F = F_{med} \\
&Fractile_{\alpha}(SSB_y / R_y, y = 1,2,...) = (SSB / R)_{eq} \quad for\ F = F_{\alpha} \\
&F_{0.9} = F_{High} \\
&F_{0.1} = F_{Low}
\end{aligned}
\tag{108}
$$

So, the observed $SSB_y/R_y$ time series is calculated, and the median found. We then find the fishing mortality for which the SSB-per-recruit is this median value based on known weight-at-age and the maturity ogive.

These reference points depend on the average state of the stock over the time period for which there are data available. These points therefore should be used with caution as they may be misleading for stocks that have been systematically over- or under- exploited for the entire period for which there are data available.

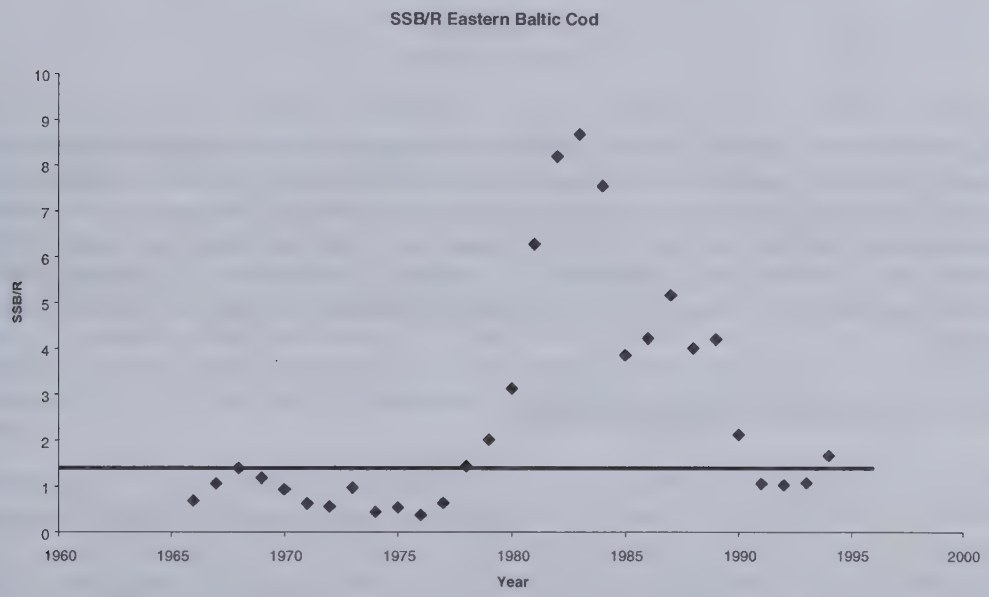


**Figure 9.6 SSB/R for the Eastern Baltic cod fishery year classes 1966-1994. The line shows the median at 1.4 kg recruit$^{-1}$ age 2. Caution is required in the interpretation as the points below the line are from one period and the points above the line from another, suggesting that the productivity of the stock has not been stable during the period for which data are available. The estimated median of 1.4 kg recruit$^{-1}$ age 2 is then taken forward into a yield per recruit model (Figure 9.7).**

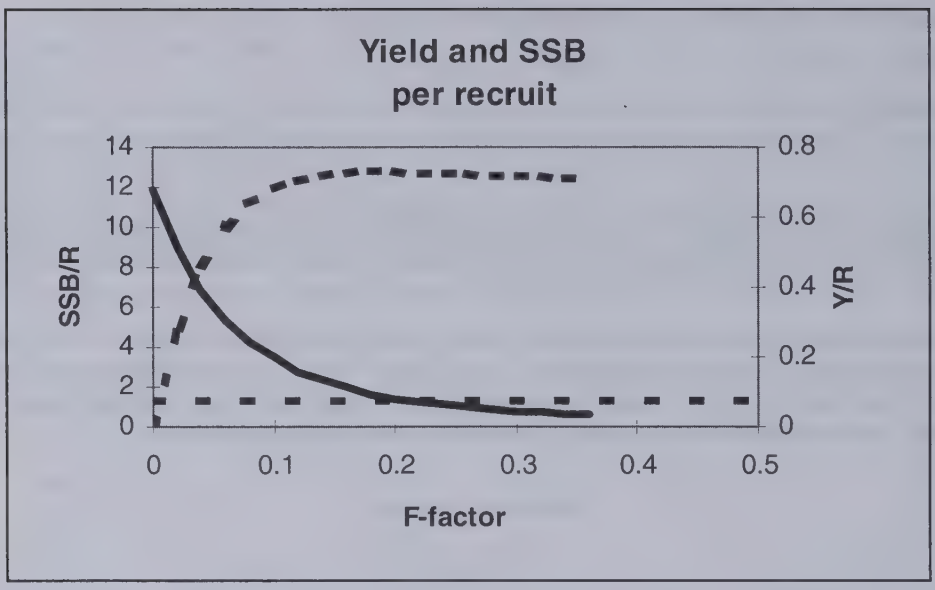


**Figure 9.7 Yield and SSB per recruit for changing F in the Eastern Baltic cod fishery. The line parallel to the x-axis is the SSB/R = 1.4; this line intersects the SSB/R (from the yield per recruit model) at an $F$ -factor (relative to the 1996 exploitation pattern) at 0.2. The process can also be done numerically by solving the definition equations for $F$. The $F_{high}$ and the $F_{low}$ are found by a similar construction, but using the 90 and 10 percentiles instead of the median SSB/R.**

### *9.5.1.4 Risk-Defined Reference Points*

Risk-defined reference points, based on the fishing mortality, are mortality values where the probability of observing the SSB (or another stock indicator) below a threshold is less than $\alpha$ %. The probability is calculated for a long time series, e.g. 100 years. The calculations are therefore to start with a stock composition, project this stock composition under a fixed fishing mortality regime for, say 100 years and use a stochastic stock-recruitment model to generate the recruitment and each year in the projection record the relevant stock indicator. This calculation is then repeated perhaps 100 times. Then, the frequency of the stock indicator falling below the set threshold is counted. This is done for several values of the fishing mortality and through iteration the reference point is derived (Figure 9.8).

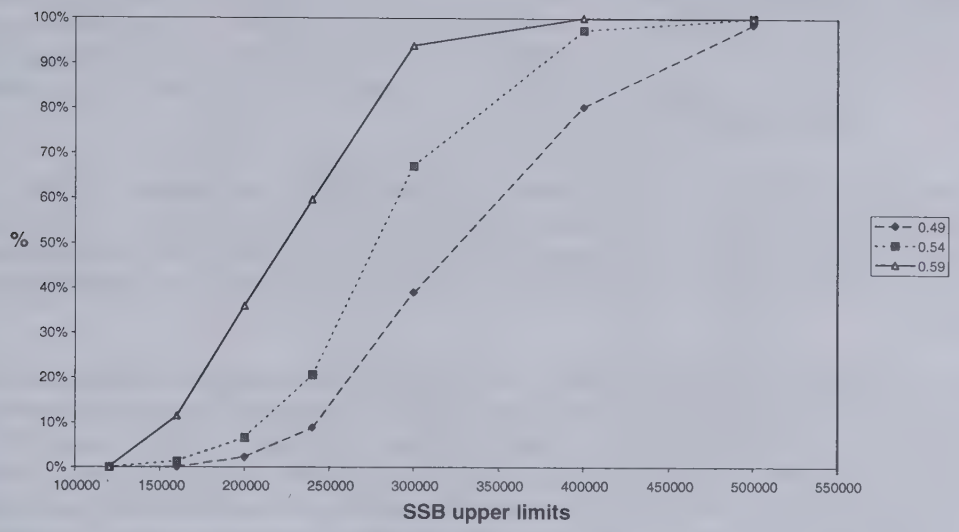


**Figure 9.8 SSB cumulative frequency distribution from a Monte Carlo simulation series. In the example, based on the Eastern Baltic Cod, three series were simulated based on fishing mortality corresponding to 1, 1.1 and 1.2 times the $F_{96}$ (i.e. with the average $F$ (age 4-7) levels of 0.49, 0.54 and 0.59). The simulation time series was 228 years, and the first 20 years after seeding with the estimated 1996 stock were ignored. The MBAL (SSB) level is usually set around 240 000 t and the graph suggests that an $F_{25\%}$ corresponding to this value is around the mid-value of the three (F(4-7) = 0.54 year$^{-1}$). These simulations were based on a B&H stock-recruitment relations fitted on the year classes 1993 –1994 to avoid an apparent shift in stock productivity in the early 1980s.**

## 9.6 FRAMEWORK FOR ADVICE

If fishery management decisions lead to $F_{pa}$ being exceeded, then this should be regarded as overfishing and management of the fishery would not be consistent with a precautionary approach. The development of a management plan to reduce fishing mortality to no greater than $F_{pa}$ should be advised.

In general, $B_{pa}$ is the biomass threshold triggering advice for a reduction in $F$ to a value below $F_{pa}$. This would depend, however, on the probability of recovering to above $B_{pa}$ in the short term using current $F_{pa}$. If SSB were predicted to remain below $B_{pa}$ in the short to medium term, the development of a recovery plan would be advised.

$F_{pa}$ and $B_{pa}$ are the main devices in the ICES framework for providing advice. They are thresholds which constrain advice or which trigger advice for the implementation of management/recovery plans.

# 10 EXAMPLES

## 10.1 INTRODUCTION

Simulated data is used for these examples. This has the advantage that the true parameters and models that produce the data are known. Hence, any structural errors in the assessments are known and data is recorded with complete accuracy. All errors stem from observation errors, which are log-normal and relatively large, however.

By introducing new data and models, we show how increasingly complex, but more realistic models can be fitted to fisheries data. We start by considering models of single cohorts, where many of the basic modelling techniques are introduced. Cross-cohort models are then discussed mainly as separable VPA. We then consider generalised linear models as structured link models and how ANOVA techniques may be used to study the structure in complex models and some use of weights in allowing different data sets to be linked to the same parameters. Finally, we show how Monte Carlo simulation techniques can be used to assess the uncertainty of the results.

The examples are developed for Microsoft Excel, using Visual Basic for Applications and the add-in optimiser, Solver. Other spreadsheet software could equally well be used.

## 10.2 SINGLE COHORT

### 10.2.1 No Abundance Index

The cohort model is based on the principle that if we know how many fish died from natural causes and we know how many were caught, we can reconstruct the history of the cohort (Table 10.1).

We need to give the final population size (or terminal F) for backward calculation, or recruitment (or initial F) for forward calculation. In this case, the Newton-Raphson method was used, but for variety, in the forward calculation form (see Macro 10.1). The recruitment and age-dependent natural mortality were provided as the input parameters. The population is modelled loosely on temperate water groundfish. The natural mortality figures are thought to represent reasonable levels for these species. It is often assumed that younger fish have higher mortality rates due to their smaller size, making them more vulnerable to predation.

Given the recruitment, we solve the Baranov equation (see Section 4.7 Solving the VPA Equations) to obtain the next population size, and so on down the cohort ages to the last year or age as a appropriate. The fishing mortality, $F_a$, is calculated as:

$$F_a = \frac{C_a M}{P_a - P_{a+1} - C_a} \tag{109}$$

**Table 10.1 Cohort catches ($C_a$), natural mortality ($M$), population size ($P_a$) and fishing mortality ($F_a$) calculated from the catch data and recruitment (population age 1). The plus-group "11+" $F_A$ is not calculated because it depends on contributions from other cohorts. This will be dealt with later (Section 10.3), and this age group can be ignored for now.**

| Age | $C_a$ | $M$ | Population | $F_a$ |
|---|---|---|---|---|
| 1 | 37937 | 0.80 | 560282 | 0.103 |
| 2 | 25608 | 0.35 | 227153 | 0.143 |
| 3 | 27537 | 0.25 | 138773 | 0.252 |
| 4 | 19460 | 0.20 | 83965 | 0.294 |
| 5 | 12784 | 0.20 | 51252 | 0.320 |
| 6 | 11391 | 0.20 | 30475 | 0.526 |
| 7 | 5618 | 0.20 | 14750 | 0.539 |
| 8 | 2641 | 0.20 | 7046 | 0.527 |
| 9 | 1253 | 0.20 | 3404 | 0.515 |
| 10 | 647 | 0.20 | 1665 | 0.553 |
| 11+ | 726 | 0.20 | 785 | |

**Macro 10.1 Visual Basic function for solving the forward VPA equations. The function requires three parameters: natural mortality ($M$), catch ($C_a$) and initial population size (Na_1). The time unit is implicit in the parameters, so the catch and natural mortality refer to the same unit of time. In contrast to the backward calculation, trial values for Na_1 maybe negative which will cause an error. More code is required to trap these (see Appendix), making the forward calculation less efficient.**

```
Function SolFVPANR(M, Ca, Na As Double) As Double
Dim fx, dfx, Na_1, DeltaNa, Z As Double
        'Estimate initial N(t+1) from Pope's cohort equation
Na_1 = Na * Exp(-M)                                  'Calculate N(a+1) with no fishing
DeltaNa = -Ca * Exp(-M / 2)                          'Calculate equivalent deaths
                                                     due to fishing
Do While Abs(DeltaNa) > 0.1                          'Test current accuracy
  Na_1 = Na_1 + DeltaNa                              'Add correction to N(t+1)
  Z = Log(Na) - Log(Na_1)                            'Calculate total mortality
  fx = (1 - M / Z) * (Na – Na_1) – Ca                'Calculate the function
  dfx = -1 + (Z - (Na – Na_1) / Na_1) * M / (Z * Z)  'And its derivative
  DeltaNa = -fx / dfx                                'Calculate the new correction
                                                     factor
Loop
SolFVPANR = Na_1                                     'Return solution
End Function
```

It is worth noting that from the model stand-point, there is no difference between using recruitment or final population size as the parameter. The only reason for using the final population size or, more often, terminal $F$, is that it is often felt that a more accurate guess can be given for this parameter than for recruitment. This decision on

parameterisation is less critical when fitting to an abundance index, but still may be useful in deciding on a starting point for the parameter for fitting purposes.

In this case, the recruitment, $M$ and all catches are known from the simulation. By using these values, we are simply repeating the simulation backwards, so the result is exact. Of course, in practice we would not know the recruitment or natural mortality exactly. In these examples, we will not be concerned with estimating natural mortality, but we will look in detail at the problem of estimating recruitment. It is worth remembering that the resulting view given by the examples will be optimistic. In practice natural mortality is never known, and may well vary with time and age.

One final point, which also applies to all further examples as well, is the implicit time unit in the mortality rates. If the time units vary, we simply multiply the rates by the new time unit in the model. Hence for all the references to $F$ and $M$ in the models below could be expanded to allow different time periods, as:

$$F \equiv Ft$$
$$M \equiv Mt \qquad (110)$$
$$\text{where} \quad \text{here} \quad t = 1$$

### 10.2.2 One Abundance Index

In cases where the final population size in the last age group is unknown, we need to estimate it. In many cases, there is additional data besides catches, which can be used as an abundance index. Here we introduce some additional data representing a scientific survey carried out in the third quarter of each year.

The timing of the index is critical where there is a significant change of population size within the season. Even if there is not thought to be a big change in population size, this is a simple adjustment to make and therefore it should not be neglected. For this simulated survey, the population must be adjusted to the number in July-September, approximately the point in time when the survey was conducted.

The population model is fitted by minimising the squared difference between the observed and expected index, the expected index being based on the population model. We therefore need to develop a link model, which will allow the expected index to be calculated from the population model. Because this is a scientific survey, it is assumed that the sampling design will ensure the index will be proportional to the population size.

We estimate the mean of the abundance index for each parameter as:

$$I_a = qP_a = qP_{a+1}e^{F_a+M} \qquad (111)$$

To fit the model, we need to be able to calculate the differential equations with respect to each of the parameters, so that we can calculate the covariance (inverse Hessian) matrix on each iteration. The first point we can note is that, as the population size is proportional to the index, the slope is equal to the population size, so:

$$\frac{\partial I_a}{\partial q} = P_a \tag{112}$$

The analysis is a little more complicated for the other parameter, the terminal population size ($P_A$). In this case, we can only define the partial differential with respect to future populations, moving towards the terminal population. Noting that $F_a$, unlike catches and natural mortality, depends on the population estimates (Equation 109), we find:

$$\frac{\partial I_a}{\partial P_A} = qP_{a+1}e^{F_a+M}\frac{\partial F_a}{\partial P_A} + q\frac{\partial P_{a+1}}{\partial P_A}e^{F_a+M} \tag{113}$$

From Equation 109, we can define the differential with respect to $F_a$ as:

$$\frac{\partial F_a}{\partial P_A} = -\frac{F_a}{(P_a - P_{a+1} - C_a)}\left(\frac{\partial P_a}{\partial P_A} - \frac{\partial P_{a+1}}{\partial P_A}\right) \tag{114}$$

By substituting Equation 114 into Equation 113 and rearranging, we find the recursive differential equation:

$$\frac{\partial I_a}{\partial P_A} = q\frac{P_a - P_{a+1}(1-F_a) - C_a}{P_a - P_{a+1}\left(1 - F_a e^{F_a+M}\right) - C_a}e^{F_a+M}\frac{\partial P_{a+1}}{\partial P_A} \tag{115}$$

The least-squares partial differentials with respect to each of the parameters is given by:

$$\begin{aligned}\frac{\partial L}{\partial P_A} &= -2\sum_{a=1}^{A}\left(I_a^{obs} - I_a\right)\frac{\partial I_a}{\partial P_A}\\ \frac{\partial L}{\partial q} &= -2\sum_{a=1}^{A}\left(I_a^{obs} - I_a\right)\frac{\partial I_a}{\partial q}\end{aligned} \tag{116}$$

where $I_a^{obs}$ is the observed index value.

We can calculate the value for each differential equation at each age, and therefore define the approximation of the least-squares (approximate) Hessian matrix as:

$$\{H\}_{P_A,q} = 2\begin{Bmatrix}\sum_{a=1}^{A}\left(\frac{\partial I_a}{\partial P_A}\right)^2 & \sum_{a=1}^{A}\frac{\partial I_a}{\partial P_A}\frac{\partial I_a}{\partial q}\\ \sum_{a=1}^{A}\frac{\partial I_a}{\partial P_A}\frac{\partial I_a}{\partial q} & \sum_{a=1}^{A}\left(\frac{\partial I_a}{\partial q}\right)^2\end{Bmatrix} \tag{117}$$

The inverse of this matrix is the covariance matrix, and can be used in the non-linear fitting process. We are now ready to apply the Newton-Raphson method, using the Hessian matrix to move towards the minimum point, where the partial differentials (Equation 116) are zero. The scheme here is:

$$\begin{Bmatrix} P_A \\ q \end{Bmatrix}^{new} = \begin{Bmatrix} P_A \\ q \end{Bmatrix} - \{H\}^{-1}_{P_A,q} \begin{Bmatrix} \frac{\partial L}{\partial P_A} \\ \frac{\partial L}{\partial q} \end{Bmatrix} \quad (118)$$

The table containing the calculations for Equation 118 can be set up in a spreadsheet (Table 10.2).

**Table 10.2 Final results of the table fitting the VPA population model to the observed abundance index. The error is the difference between the observed index and the index estimated from the model (i.e. $I_a^{obs}$-$I_a$). Notice, the differential $dI_a/dq$ is identical to the population size, $P_a$. As in the previous analysis, the 11+ group is ignored as it contains animals from other cohorts not modelled here.**

| Linear Index | | | | | $P_A$ | 4624.22 | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | $q$ | $1.03\ 10^{-5}$ | | | | |
| **Age** | $C_a$ | $I_a^{obs}$ | $M$ | $P_a$ | $F_a$ | $I_a$ | **Error** | **(Error)$^2$** | $dI_a/dP_A$ | $dI_a/dq$ |
| 1 | 37937 | 6.3974 | 0.80 | 600773 | 0.096 | 6.187 | 0.211 | 0.044 | 13.622 | $6.008\ 10^5$ |
| 2 | 25608 | 1.7395 | 0.35 | 245336 | 0.132 | 2.526 | -0.787 | 0.619 | 6.117 | $2.453\ 10^5$ |
| 3 | 27537 | 1.6226 | 0.25 | 151579 | 0.229 | 1.561 | 0.062 | 0.004 | 4.308 | $1.516\ 10^5$ |
| 4 | 19460 | 1.7253 | 0.20 | 93927 | 0.258 | 0.967 | 0.758 | 0.575 | 3.352 | $9.393\ 10^4$ |
| 5 | 12784 | 0.4771 | 0.20 | 59398 | 0.270 | 0.612 | -0.135 | 0.018 | 2.741 | $5.940\ 10^4$ |
| 6 | 11391 | 0.2721 | 0.20 | 37134 | 0.410 | 0.382 | -0.110 | 0.012 | 2.242 | $3.713\ 10^4$ |
| 7 | 5618 | 0.1729 | 0.20 | 20183 | 0.364 | 0.208 | -0.035 | 0.001 | 1.830 | $2.018\ 10^4$ |
| 8 | 2641 | 0.0559 | 0.20 | 11480 | 0.291 | 0.118 | -0.062 | 0.004 | 1.495 | $1.148\ 10^4$ |
| 9 | 1253 | 0.0255 | 0.20 | 7025 | 0.218 | 0.072 | -0.047 | 0.002 | 1.222 | $7.025\ 10^3$ |
| 10 | 647 | 0.0173 | 0.20 | 4624 | 0.033 | 0.048 | -0.030 | 0.001 | 1.000 | $4.624\ 10^3$ |
| 11+ | 726 | 0.0142 | 0.20 | | | | | | | |
| | | | | | | | Sum | 1.281 | | |
| | | | | | | | df | 8 | | |

The table can be used to calculate the Hessian and vector of partial differentials required for the Newton-Raphson method (Equation 118).

**Table 10.3 The Hessian matrix, its inverse (covariance matrix) and the parameter vectors calculated from Table 10.2. The parameters are taken at their minimum, so the $\partial L/\partial P_A$ and $\partial L/\partial q$ differentials are relatively close to zero (with respect to their variances). The Net Change from multiplying the differential by the covariance matrix is very small, indicating convergence. Hence the New $P_A$ and $q$ do not change significantly from those in Table 10.2. Note that the correlation between the parameters is very high, so an estimate for either of the parameters will be accurate only if the other parameter is known.**

| Hessian Matrix | $P_A$ | $q$ |
|---|---|---|
| $P_A$ | 546.7635 | 21931023.2 |
| $q$ | 21931023 | $9.169\ 10^{+11}$ |

| Covariance Matrix | $P_A$ | $q$ |
|---|---|---|
| $P_A$ | 0.04507753 | $-1.0782\ 10^{-06}$ |
| $q$ | $-1.0782\ 10^{-06}$ | $2.6881\ 10^{-11}$ |

Correlation -0.980

| | $\partial L$ | Net Change |
|---|---|---|
| $\partial P_A$ | 0.000 | $4.443\ 10^{-6}$ |
| $\partial q$ | -4.821 | $-1.115\ 10^{-10}$ |

| | New |
|---|---|
| $P_A$ | 4624.22 |
| $q$ | 1.03E-05 |

Repeatedly placing the new values for the parameters from Table 10.3 back into the calculation Table 10.2 can be done manually or through a macro, until convergence. If you try implementing the method above, starting from arbitrary parameter values you will notice that the $q$ estimate is found very quickly, whereas the $P_A$ estimate converges very slowly, too slowly for the method to be useful. If you try the Solver routine, the least-squares estimate will be found for both parameters very quickly. This is because Solver uses a more sophisticated technique, where the Newton-Raphson method is only one method out of several ways it will move towards the solution. However, although it is more robust, using Solver gives us no clues as to whether the model fits.

The fact that the fitting process behaved poorly should sound some alarm bells. The model may need looking at in more detail. One clear indication is the errors in Table 10.2 are larger for the larger population size. This is strongly indicative of changing variance and skewed errors, which may be corrected by a transformation. We try the same routine, but with a log-transform below.

A log-transform can be undertaken by simply redefining the models in terms of log-values. We now have:

$$\Pi_a = Ln(P_a) = \Pi_{a+1} + F_a + M$$
$$J_a = Ln(I_a) = Ln(q) + \Pi_a \quad (119)$$

We need to estimate the parameters in their log form, that is the index parameter $Ln(q)$, and the terminal log-population $\Pi_A$. The two partial differentials can be derived through the same process as that described for the linear index:

$$\frac{\partial J_a}{\partial Ln(q)} = 1 \quad (120)$$

$$\frac{\partial J_a}{\partial \Pi_A} = \frac{P_a - P_{a+1}(1-F_a) - C_a}{P_a(1+F_a) - P_{a+1} - C_a} \frac{\partial J_{a+1}}{\partial \Pi_A} \quad (121)$$

Otherwise, the method is identical. The calculation Table 10.4 for the fitted model indicates the errors are well behaved, so the largest errors are not associated with the larger populations. Also, the parameter correlation has been much reduced (Table 10.5), so there is less dependency between parameter estimates. The true parameter values known from the simulation suggest that while the $q$ estimate is a little further away from its true value ($1.0\ 10^{-5}$), the terminal population size is much closer to the true value of 1665 (from Table 10.1).

**Table 10.4 Final results of the table fitting the VPA population model to the observed log abundance index. The error is the difference between the observed log-index and the index estimated from the model (i.e. $J_a^{obs}$-$J_a$). The differential $dJ_a/dLn(q)$ is always equal to 1.0, and therefore not included in this table.**

| Log Model | | | | | | | Log$_e$ | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | $\Pi_A$ | 1336 | 7.197 | | | |
| | | | | | $q$ | $1.081\ 10^{-5}$ | -11.435 | | | |
| **Age** | $C_a$ | $J_a^{obs}$ | $M$ | $P_a$ | $\Pi_a$ | $F_a$ | $J_a$ | **Error** | **(Error)$^2$** | $dJ_a/d\Pi_A$ |
| 1 | 37937 | 1.8559 | 0.80 | 555729 | 13.228 | 0.104 | 1.793 | 0.063 | 0.004 | 0.033 |
| 2 | 25608 | 0.5536 | 0.35 | 225109 | 12.324 | 0.144 | 0.889 | -0.336 | 0.113 | 0.037 |
| 3 | 27537 | 0.4840 | 0.25 | 137333 | 11.830 | 0.255 | 0.395 | 0.089 | 0.008 | 0.043 |
| 4 | 19460 | 0.5454 | 0.20 | 82846 | 11.325 | 0.298 | -0.110 | 0.656 | 0.430 | 0.055 |
| 5 | 12784 | -0.7400 | 0.20 | 50337 | 10.826 | 0.327 | -0.609 | -0.131 | 0.017 | 0.074 |
| 6 | 11391 | -1.3017 | 0.20 | 29727 | 10.300 | 0.543 | -1.135 | -0.166 | 0.028 | 0.102 |
| 7 | 5618 | -1.7549 | 0.20 | 14140 | 9.557 | 0.570 | -1.878 | 0.123 | 0.015 | 0.175 |
| 8 | 2641 | -2.8845 | 0.20 | 6550 | 8.787 | 0.581 | -2.648 | -0.237 | 0.056 | 0.308 |
| 9 | 1253 | -3.6709 | 0.20 | 3000 | 8.006 | 0.609 | -3.429 | -0.242 | 0.059 | 0.547 |
| 10 | 647 | -4.0569 | 0.20 | 1336 | 7.197 | 0.188 | -4.238 | 0.181 | 0.033 | 1.000 |
| 11+ | 726 | -4.2515 | 0.20 | | | | | | | |
| | | | | | | | | Sum | 0.762 | |
| | | | | | | | | df | 8 | |

**Table 10.5 The Hessian matrix, its inverse (covariance matrix) and the parameter vectors calculated from Table 10.4. The correlation between the parameters is still high, but much reduced from the poorer normal least-squares fit (Table 10.3).**

| Hessian Matrix | $\Pi_A$ | $Ln(q)$ |
|---|---|---|
| $\Pi_A$ | 2.8962 | 4.7479 |
| $Ln(q)$ | 4.7479 | 20 |

| Covariance Matrix | $\Pi_A$ | $Ln(q)$ |
|---|---|---|
| $\Pi_A$ | 0.5653 | -0.1342 |
| $Ln(q)$ | -0.1342 | 0.08186 |

Correlation -0.624

| | $\partial L$ | Net Change |
|---|---|---|
| $\partial \Pi_A$ | 0.000 | $3.961\ 10^{-7}$ |
| $\partial Ln(q)$ | 0.000 | $-1.267\ 10^{-7}$ |

| | New |
|---|---|
| $\Pi_A$ | 7.197 |
| $Ln(q)$ | -11.435 |

Using the log fit above we find the method works well and finds the solution in as many iterations as Solver. The index was simulated using the log-normal, so we happen to know this method is correct, which can also be verified by inspecting plots of the residuals. As a rule of thumb, the fitting method tends to work when the model fits the data well (although this is not the only criterion). Problems with the numerical technique is often a symptom of an underlying poor model, a fact that may be missed using black-box minimising routines.

Finally, we consider the correction for timing of the observation. This requires that the population size is adjusted to represent the mean population size during the survey.

$$J_a = \ln q + \tau_a + \Pi_a = \ln q + \tau_a + \Pi_{a+1} + F_a + M \tag{122}$$

The proportional decrease in mean population size is derived from integration over the period of the survey:

$$\tau_a = -\alpha(F_a + M) + \ln\left(\frac{1 - e^{-(\beta-\alpha)(F_a+M)}}{(\beta-\alpha)(F_a+M)}\right) \tag{123}$$

Again the procedure is exactly the same as that presented above. However, we do need to adjust the partial differential with respect to the terminal population size ($dJ_a/dP_A$) to account for the within season changes:

$$\frac{\partial J_a}{\partial \Pi_A} = \frac{\partial \tau_a}{\partial \Pi_A} + \frac{\partial \Pi_{a+1}}{\partial \Pi_A} + \frac{\partial F_a}{\partial \Pi_A} \tag{124}$$

$$= \frac{\partial \Pi_{a+1}}{\partial \Pi_A} + \frac{\partial F_a}{\partial \Pi_A}\left(1-\alpha-\frac{1}{F_a+M}+\frac{(\beta-\alpha)e^{-(\beta-\alpha)(F_a+M)}}{1-e^{-(\beta-\alpha)(F_a+M)}}\right)$$

where (125)

$$\frac{\partial F_a}{\partial \Pi_A} = \frac{-F_a}{e^{\Pi a}-e^{\Pi a+1}-C_a}\left(e^{\Pi a}\frac{\partial \Pi_a}{\partial \Pi_A} - e^{\Pi a+1}\frac{\partial \Pi_{a+1}}{\partial \Pi_A}\right)$$

A brief perusal of this equation explains why numerical approximations of the differential are popular. The equations become very complicated as models become more realistic. However, the fitting procedure remains the same whether $dJ_a/d\Pi_A$ is estimated numerically or calculated using Equation 125.

**Table 10.6 Final results of the table fitting the VPA population model to the observed log abundance index, adjusted for timing of the survey during the season. The differential $dJ_a/dLn(q)$ is always equal to 1.0, and therefore not included in this table. *Note that in contrast to the previous models, it was not necessary to know the fishing mortality for the final age class ($F_{10}$). However, to adjust the index for survey timing it is required. In this case, it was assumed to be the same as the fishing mortality in the previous age class ($F_{10}= F_9$), the alternative option being to ignore the final age class's index ($J_{10}$).**

| Log Model | | | | | Log$_e$ | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Index adjusted | | | $\Pi_A$ | | 1460 | 7.286 | | $\alpha$ | 0.50 | |
| | | | $q$ | | 1.316 $10^{-5}$ | -11.238 | | $\beta$ | 0.75 | |
| **Age** | $C_a$ | $J_a^{obs}$ | $M$ | $\Pi_a$ | $F_a$ | $\tau$ | $J_a$ | **Error** | $d\Pi_a/d\Pi_A$ | $dJ_a/d\Pi_A$ |
| 1 | 37937 | 1.3569 | 0.80 | 13.231 | 0.103 | -0.5625 | 1.431 | -0.074 | 0.036 | 0.039 |
| 2 | 25608 | 0.3329 | 0.35 | 12.328 | 0.144 | -0.3079 | 0.782 | -0.449 | 0.040 | 0.044 |
| 3 | 27537 | 0.3250 | 0.25 | 11.834 | 0.254 | -0.3145 | 0.282 | 0.043 | 0.046 | 0.055 |
| 4 | 19460 | 0.4153 | 0.20 | 11.330 | 0.296 | -0.3097 | -0.218 | 0.633 | 0.060 | 0.072 |
| 5 | 12784 | -0.8841 | 0.20 | 10.833 | 0.324 | -0.3268 | -0.732 | -0.153 | 0.080 | 0.099 |
| 6 | 11391 | -1.4677 | 0.20 | 10.309 | 0.536 | -0.4588 | -1.388 | -0.080 | 0.111 | 0.159 |
| 7 | 5618 | -1.9230 | 0.20 | 9.573 | 0.557 | -0.4719 | -2.137 | 0.214 | 0.188 | 0.274 |
| 8 | 2641 | -3.0542 | 0.20 | 8.815 | 0.559 | -0.4731 | -2.896 | -0.158 | 0.327 | 0.477 |
| 9 | 1253 | -3.8417 | 0.20 | 8.056 | 0.570 | -0.4795 | -3.662 | -0.180 | 0.569 | 0.837 |
| 10 | 647 | -4.2285 | 0.20 | 7.286 | 0.570* | -0.4795 | -4.431 | 0.203 | 1.000 | 0.837 |
| 11+ | 726 | -4.4232 | 0.20 | | | | | | | |
| | | | | | | **Sum Squares** | | 0.784 | | |
| | | | | | | **df** | | 8 | | |

### 10.2.3 Uncertain Catch

Up to now we have assumed that the catch is known exactly. In practice, the catch may be estimated like any other model variable. To represent this, we need an additional sum-of-squares term adding up the squared difference between the observed catch and the catch estimated by the model. The full Newton-Raphson method above can be implemented in the same way, we just have to remember to find the partial differential with respect to each parameter for each sum-of-squares term separately.

We can set up the problem as in the case where we have an abundance index using the procedures described above. Now instead of having a single sum-of-squares, we have two. One for the index as above, but a second for the log catches:

$$L = \sum_{a=1}^{A} \left(\ln\left(C_a^{obs}\right) - \ln(C_a)\right)^2 + \lambda_J \sum_{a=1}^{A} \left(J_a^{obs} - J_a\right)^2$$
$$\frac{\partial L}{\partial \Pi_a} = -2\left(\ln\left(C_a^{obs}\right) - \ln(C_a)\right)\frac{\partial \ln(C_a)}{\partial \Pi_a} - 2\lambda_J \left(J_a^{obs} - J_a\right)\frac{\partial J_a}{\partial \Pi_a} \quad (126)$$

where

$$\frac{\partial \ln(C_a)}{\partial \Pi_a} = \frac{F_a(F_a + M)P_a - M(P_a - P_{a+1})}{F_a(F_a + M)(P_a - P_{a+1})}$$
$$\frac{\partial J_a}{\partial \Pi_a} = 1 \quad (127)$$

We now have all the $\Pi_a$ as parameters, not just $\Pi_A$. Equations 126 and 127 can be used with the other differentials ($dC_a/d\ln(q)$ = 0; $dJ_a/d\ln(q)$ = 1.0) to calculate the covariance matrix as in the previous analyses. However, if you try this you are likely to be disappointed. The matrix is close to singular, and the inversion routine available in a spreadsheet gives very inaccurate results. Better routines could be used in a dedicated computer program, but for this demonstration Solver is quite adequate and will find the minimum. In general, the method of solving the normal equations by matrix inversion as described in this manual works best for small numbers of parameters and only where matrices are not close to being singular. It nevertheless remains a useful technique for linear sub-models, as demonstrated later.

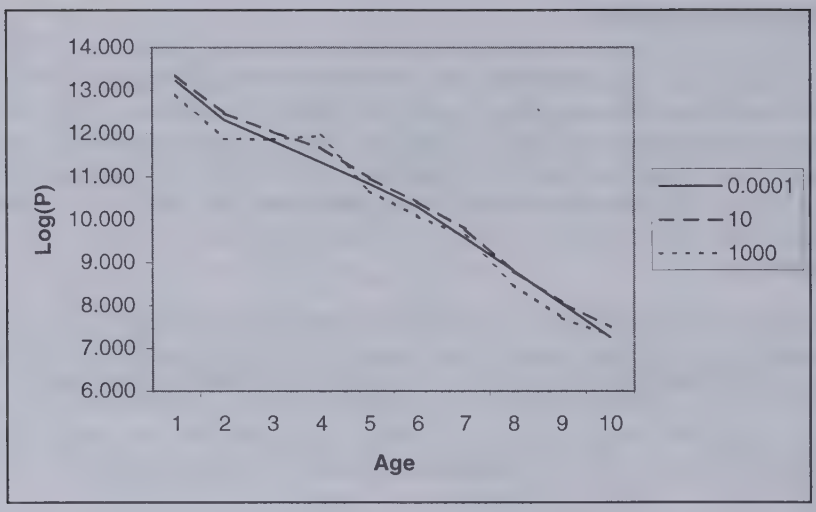


**Figure 10.1 Illustration of the effect of the series weighting parameter ($\lambda_J$ ) on population estimates. When the parameter is small, the relative weight given to the catch series is large and the fit is very similar to the VPA model, where the population is back-calculated exactly. As this weight is increased, the model follows the abundance index more closely, and the catches do not fit exactly. In the extreme case ($\lambda_J$=1000), the population actually increases from age 3 to 4 ignoring the population model altogether.**

Notice that when the abundance index is not used, the difference between the observed and model catches can be reduced to zero. Including the abundance index produces a balance between the index and the catch link models in distributing the error between them. The balance is controlled by the $\lambda_J$ parameter (Figure 10.1), which is, essentially, the ratio between the variances of the catch and index series. As the $\lambda_J$ weight approaches zero, the standard VPA fits are reproduced as above. Conversely, as the parameter increases in size, the fit favours the abundance index, which the estimated population sizes will begin to resemble. Weighting heavily in favour of the index can lead to, for instance, increases in the population through time, essentially ignoring catches and the population model altogether. For this reason, the index is usually assumed to have lower weight compared to catches. If this is not the case, some other method will be needed to constrain the population size to realistic levels dictated by the population model.

This illustrates an important concept in stock assessment. The way the fishing activities impact the ecosystem in stock assessment is through catches. Other forms of impact, such as habitat degradation, need to be considered separately. Therefore, only catches appear in the population model. As long as they are correctly measured, fluctuations in population size brought about by fishing will be correctly determined. If they are not well measured, these fluctuations will add to the process errors. If fishing is having the largest single impact on the population, these introduced errors may be large, causing the results to be poor. Accurate catch data is therefore more important than effort or index data.

## 10.3 MULTIPLE COHORTS

Why combine cohorts into complicated-looking matrices rather than analyse each cohort separately? In the matrix form, the cohorts run diagonally through, each cohort remains entirely separate, and the models presented above could be fitted to each individually. Unless we build linkages across cohorts, there is no difference between fitting the VPA to separate cohorts and to the full cohort matrix. In matrix form, we can simply work back along each cohort, fitting each terminal $F$ parameter separately. The reason for combining cohorts is to link the cohort models by sharing parameters between them. This will make parameter estimates more accurate.

As already mentioned, the plus-group can be modelled through multiple cohorts. This is of limited value, as the plus-group is usually chosen to be a trivial part of the catch. Of greater importance is to share any index parameters across cohorts. We are also able to construct new models, such as the separable VPA described below.

### 10.3.1 Separable VPA

In separable VPA, we reduce the number of fishing mortality parameters by building a model of fishing mortality that applies across cohorts. This means the model no longer exactly fits and the exact solution to the Baranov catch equation no longer applies. Instead, we use the least-squares method to find the best fit between the observed (Table 10.7) and expected catches. In this formulation, the link model describes the relationship between the observed and expected catches, and the population model contains no data at all to drive it.

**Table 10.7 Total catches recorded for all cohorts 1984-1994. Example catches used in the single cohort analyses above are highlighted by shaded cells.**

| Age | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 37937 | 25689 | 54983 | 96100 | 100014 | 155100 | 21200 | 56188 | 109213 | 36688 | 60240 |
| 2 | 27434 | 25608 | 17914 | 41556 | 68278 | 91377 | 114110 | 16660 | 42978 | 83706 | 36624 |
| 3 | 33684 | 31166 | 27537 | 16162 | 49154 | 81395 | 76090 | 81639 | 13066 | 29373 | 83690 |
| 4 | 20954 | 25082 | 22149 | 19460 | 14370 | 28193 | 48909 | 37360 | 53083 | 6860 | 26475 |
| 5 | 10266 | 11952 | 10270 | 21132 | 12784 | 9157 | 14879 | 29597 | 23121 | 32506 | 6124 |
| 6 | 6559 | 7698 | 8029 | 5790 | 7615 | 11391 | 5222 | 9278 | 14256 | 14064 | 24978 |
| 7 | 3161 | 3210 | 4936 | 4623 | 4786 | 6028 | 5618 | 2592 | 5001 | 8068 | 8544 |
| 8 | 1178 | 2062 | 2459 | 2568 | 2889 | 3182 | 2719 | 2641 | 1407 | 2706 | 4370 |
| 9 | 689 | 1116 | 1050 | 1349 | 929 | 1330 | 1410 | 1309 | 1253 | 643 | 1639 |
| 10 | 452 | 552 | 577 | 583 | 644 | 579 | 621 | 627 | 645 | 647 | 399 |
| 11+ | 453 | 545 | 628 | 616 | 643 | 789 | 586 | 608 | 569 | 576 | 726 |

The basic population model is the back-calculated equation:

$$P_a = P_{a+1} e^{F_{ay}+M_a} \tag{128}$$

The $F_{ay}$ parameters now depend upon the separable VPA model:

$$F_{ay} = S_a E_y \tag{129}$$

where $E_y$ is the yearly exploitation rate. To avoid over-parameterisation, $E_y$ can be chosen so that it is fishing mortality for the base age, and $S_a$ represents relative departures from this level (Table 10.8), or similar methods. We can avoid the need for additional parameters by defining the terminal $F$ parameters using the same model. So, for the current analysis:

$$\begin{aligned} F_{10,y} &= E_y \\ P_{10,y} &= \frac{C_{10,y}}{\left(1-e^{-E_y-M_{10}}\right)} \frac{\left(E_y+M_{10}\right)}{E_y} \end{aligned} \tag{130}$$

and

$$P_{a,1994} = \frac{C_{a,1994}}{\left(1-e^{-S_a E_{1994}-M_a}\right)} \frac{\left(S_a E_{1994}+M_a\right)}{S_a E_{1994}}$$

We could also use the estimated $F_{11,y}$ to define the plus-group population size in the same way, although this wastes the observed catch data for this group. Instead, we can define a model where this group accumulates survivors from the cohorts:

$$P_{11,y} = \left(P_{11,y+1} - P_{10,y+1} e^{F_{10,y}+M_a}\right) e^{F_{11,y}+M_a} \tag{131}$$

Therefore, for any set of exploitation rates $E_y$ and selectivity coefficients $S_a$, we can define the full matrix of population sizes and, more importantly catches through the Baranov catch equation. The task is to minimise the difference between these model log-catches and the observed log-catches by least-squares.

Comparing the estimated $F_{ay}$ to the true $F_{ay}$ generated by the simulation indicates much poorer estimates towards the end of the time series. This is always a problem with VPA techniques. The estimates are more accurate further back in time as there are more observations made on each of the cohorts. So, for example, the 1994 age 1 cohort has only one set of catches so the estimated $F_{1,1994}$ is very unreliable. In contrast, the selectivity estimates, which makes use of data right across the matrix, are fairly good (Table 10.8).

**Table 10.8 Fishing mortality estimated from the separable VPA model. The shaded cells contain the parameters used in the model and estimated by Solver. Comparison with the true parameters indicates that the selectivity is well estimated ($r^2$=0.93) compared to the exploitation rate ($r^2$=0.21).**

| Age | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | $S_a$ | $M_a$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 0.09 | 0.11 | 0.11 | 0.11 | 0.11 | 0.12 | 0.11 | 0.10 | 0.09 | 0.08 | 0.08 | 0.26 | 0.80 |
| 2 | 0.15 | 0.17 | 0.18 | 0.18 | 0.18 | 0.20 | 0.18 | 0.17 | 0.15 | 0.13 | 0.13 | 0.42 | 0.35 |
| 3 | 0.24 | 0.28 | 0.29 | 0.29 | 0.29 | 0.32 | 0.29 | 0.27 | 0.24 | 0.21 | 0.21 | 0.68 | 0.25 |
| 4 | 0.29 | 0.33 | 0.34 | 0.34 | 0.35 | 0.37 | 0.34 | 0.31 | 0.28 | 0.25 | 0.25 | 0.79 | 0.20 |
| 5 | 0.32 | 0.37 | 0.38 | 0.38 | 0.38 | 0.41 | 0.38 | 0.35 | 0.31 | 0.28 | 0.28 | 0.88 | 0.20 |
| 6 | 0.35 | 0.41 | 0.42 | 0.42 | 0.43 | 0.46 | 0.42 | 0.39 | 0.34 | 0.31 | 0.31 | 0.98 | 0.20 |
| 7 | 0.36 | 0.41 | 0.43 | 0.43 | 0.43 | 0.47 | 0.43 | 0.40 | 0.35 | 0.31 | 0.31 | 1.00 | 0.20 |
| 8 | 0.36 | 0.41 | 0.42 | 0.43 | 0.43 | 0.46 | 0.42 | 0.39 | 0.35 | 0.31 | 0.31 | 0.99 | 0.20 |
| 9 | 0.37 | 0.43 | 0.44 | 0.44 | 0.45 | 0.48 | 0.44 | 0.41 | 0.36 | 0.32 | 0.32 | 1.03 | 0.20 |
| 10 | 0.36 | 0.41 | 0.43 | 0.43 | 0.44 | 0.47 | 0.43 | 0.40 | 0.35 | 0.31 | 0.31 | | 0.20 |
| 11+ | 0.31 | 0.36 | 0.37 | 0.37 | 0.38 | 0.40 | 0.37 | 0.34 | 0.30 | 0.27 | 0.27 | 0.86 | 0.20 |

An important addition would be effort data, not necessarily because the model will fit better, but because effort provides a way to forecast future states of the fishery, as effort is often controlled by management. We can fit the model above, replacing the $E_y$ in Equation 129 with effort data, but adding an additional parameter $S_{10}$, which was not required in the previous form of the model. $S_a$ now represents age-dependent catchability.

For variety, we develop a slightly different model, based upon the classical VPA population model. The same parameter set up as in Table 10.8 is used for fishing mortality. For the population model, however, we use the observed catches solving the standard VPA equation:

$$C_{ay} = \left[1 - \frac{M_a}{\ln P_{ay} - \ln P_{a+1,y+1}}\right]\left(P_{ay} - P_{a+1,y+1}\right) \qquad (132)$$

For the terminal populations, we use the terminal $F$ estimate (Equation 130) and back-calculate cohorts by solving Equation 132. However, as the plus-group accepts cohorts from the terminal population (age 10), we must use the forward VPA solution to estimate this population, adding together both the survivors from the previous year's plus group and the survivors from the new cohort (last year's age 10). For each age group in each year, we can now minimise the squared difference between

the population model estimate of the log-$F_{ay}$ with the separable estimate of the log-$F_{ay}$.

With effort data replacing the exploitation rate, only selectivity ($S_a$) needs to be estimated. This results in the population and fishing mortality being estimated reasonably well with only 10 parameters (Table 10.9). Although this separable VPA model was used in the simulation to generate the data, both fishing mortality and catch were estimated as log-normal variates, so the error remains high. As in the previous models, errors were worse for the more recent years, the ones that are usually of most interest. This problem can really only be addressed using other sources of data.

**Table 10.9 Fishing mortality estimated from the separable VPA model with effort data. The shaded cells contain the parameters used in the model and estimated by Solver. The exploitation rate is now correct as it uses the simulation effort data. Comparison with the true selectivity parameters indicates the selectivity is well estimated ($r^2$=0.88). The overall $F$ estimates are much better than when the exploitation rate was unknown, but the most inaccurate estimates remain in 1994 year.**

| | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | $S_a$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Effort** | 2100 | 2200 | 2200 | 2300 | 2500 | 3000 | 2900 | 2900 | 2900 | 2900 | 4000 | |
| **Age** 1 | 0.08 | 0.09 | 0.09 | 0.09 | 0.10 | 0.12 | 0.12 | 0.12 | 0.12 | 0.12 | 0.16 | $4.00\ 10^{-5}$ |
| 2 | 0.14 | 0.14 | 0.14 | 0.15 | 0.16 | 0.19 | 0.19 | 0.19 | 0.19 | 0.19 | 0.26 | $6.48\ 10^{-5}$ |
| 3 | 0.22 | 0.23 | 0.23 | 0.24 | 0.26 | 0.32 | 0.31 | 0.31 | 0.31 | 0.31 | 0.42 | $1.05\ 10^{-4}$ |
| 4 | 0.26 | 0.27 | 0.27 | 0.28 | 0.31 | 0.37 | 0.35 | 0.35 | 0.35 | 0.35 | 0.49 | $1.22\ 10^{-4}$ |
| 5 | 0.28 | 0.29 | 0.29 | 0.31 | 0.33 | 0.40 | 0.39 | 0.39 | 0.39 | 0.39 | 0.53 | $1.33\ 10^{-4}$ |
| 6 | 0.30 | 0.32 | 0.32 | 0.33 | 0.36 | 0.43 | 0.42 | 0.42 | 0.42 | 0.42 | 0.58 | $1.45\ 10^{-4}$ |
| 7 | 0.33 | 0.35 | 0.35 | 0.36 | 0.39 | 0.47 | 0.46 | 0.46 | 0.46 | 0.46 | 0.63 | $1.57\ 10^{-4}$ |
| 8 | 0.34 | 0.36 | 0.36 | 0.38 | 0.41 | 0.49 | 0.48 | 0.48 | 0.48 | 0.48 | 0.66 | $1.64\ 10^{-4}$ |
| 9 | 0.33 | 0.34 | 0.34 | 0.36 | 0.39 | 0.47 | 0.45 | 0.45 | 0.45 | 0.45 | 0.62 | $1.55\ 10^{-4}$ |
| 10 | 0.33 | 0.34 | 0.34 | 0.36 | 0.39 | 0.47 | 0.45 | 0.45 | 0.45 | 0.45 | 0.62 | $1.56\ 10^{-4}$ |
| 11+ | 0.25 | 0.26 | 0.26 | 0.28 | 0.30 | 0.36 | 0.35 | 0.35 | 0.35 | 0.35 | 0.48 | $1.20\ 10^{-4}$ |

### 10.3.2 Including Several Indices

We now consider the case where we have three indices of abundance. In addition to a scientific survey, as used for the single cohort, we assume we have a biomass index and the effort data used in the previous example. Rather than construct a new model, we shall use the separable VPA analysis with effort data described above (Section 10.3.1). The approach is much the same for several abundance indices as for one, however each index may have a different model linking it to the population.

For the scientific survey, we assume that sampling was organised such that we can have confidence that the relationship between the index and cohort size in each year is linear and errors are log-normal:

$$J_{ay} = \ln(q_J) + \ln(\tilde{P}_{ay}) \tag{133}$$

The timing for the index will be the third quarter of the year. The least-squares estimate of the coefficient $\ln(q_J)$ can be calculated using the normal linear least-squares techniques. In this case, the solution is very simple, it is the average difference between the log-population size and the index:

$$\ln(q_J) = \frac{\sum_{y=1}^{Y}\sum_{a=1}^{A} J_{ay}^{obs} - \sum_{y=1}^{Y}\sum_{a=1}^{A} \ln(\tilde{P}_{ay})}{AY} \tag{134}$$

We will imagine here that for the biomass index only catch weight per unit effort data were recorded, so it is related to the total biomass of the population in the year. Hence,

$$J_{By} = \ln(q_B) + v \ln\left(\sum_{a=1}^{A} w_{ay}\tilde{P}_{ay}\right) \tag{135}$$

where $w_{ay}$ is the average weight at age in each year. Weight data would probably be available from the scientific survey and catch samples. The biomass index could be obtained from another scientific survey using fishing gear or from an acoustic survey. Note that in this case we do not assume a linear relationship between the index and population size. This might be because, for example, the data was a by-product of a survey for another species, not designed to sample this species, rendering the linear relationship suspect. Also note that it may be possible to obtain, through acoustic surveys for example, an absolute estimate of the biomass which would not require an estimate of $\ln(q_B)$ or $v$. This is highly desirable as it reduces the parameters required and more importantly parameter aliasing.

Once we have calculated the population sizes at the time of the survey, and we know the average size of each age group, for any set of population parameters we can calculate the biomass in each year. This is the $x_2$ variable in the regression. The $x_1$ variable is a dummy variable for the constant term. Given the observed index, we can find the least squares solution directly by inverting the Hessian matrix. As the matrix is small, we can write out the full equations for the least-squares estimates:

$$\ln q_B = \frac{\sum_{y=1}^{Y} \mathrm{B}_y^2 \sum_{y=1}^{Y} J_{\mathrm{B}y}^{obs} - \left(\sum_{y=1}^{Y} \mathrm{B}_y\right)\left(\sum_{y=1}^{Y} \mathrm{B}_y J_{\mathrm{B}y}^{obs}\right)}{D}$$

$$v = \frac{Y\sum_{y=1}^{Y} \mathrm{B}_y J_{\mathrm{B}y}^{obs} - \sum_{y=1}^{Y} \mathrm{B}_y \sum_{y=1}^{Y} J_{\mathrm{B}y}^{obs}}{D} \qquad (136)$$

where

$$D = Y\sum_{y=1}^{Y} \mathrm{B}_y^2 - \left(\sum_{y=1}^{Y} \mathrm{B}_y\right)^2$$

Finally, we consider using the effort data. As will have been gathered, effort can be included in the assessment in a variety of ways. Perhaps most commonly, we can produce CPUE as abundance indices, and use models similar to the scientific survey or biomass link models (Equations 133 or 135). However, it is important to appreciate the variety of approaches available that may be used to adapt techniques to local fisheries and data sets. To illustrate alternatives, we use the separable VPA model to build a link between the population and the observed effort. We reverse the log form of the separable VPA model (Equation 129) to generate the expected exploitation rate from the model:

$$\ln\left(E_{ay}\right) = \ln\left(F_{ay}\right) - \ln\left(S_a\right) \qquad (137)$$

This can be compared with the observed effort in each year. The $F_{ay}$ can be calculated for each age and year by:

$$\ln\left(F_{ay}\right) = \ln\left(P_{ay}\right) - \ln\left(P_{a+1,y+1}\right) - M_a \qquad (138)$$

with the exception of the terminal years. For these, where $P_{a+1,y+1}$ is unavailable, we need to solve the Baranov catch equation for $F$ calculating forward (see Macro 10.2). Once we have the $F_{ay}$ matrix, the least-squares solution for $S_a$ parameters can be calculated as the mean difference between the log-effort and log-fishing mortality:

$$\ln\left(S_a\right) = \frac{\sum_{y=1}^{Y} \ln\left(E_{ay}\right) - \sum_{y=1}^{Y} \ln\left(F_{ay}\right)}{Y} \qquad (139)$$

The aim now is to minimise the least-squares equation:

$$L = \sum_{y=1}^{Y}\sum_{a=1}^{A}\left(E_y^{obs} - E_{ay}\right)^2 + \lambda_B \sum_{y=1}^{Y}\left(B_y^{obs} - B_y\right)^2 + \lambda_J \sum_{y=1}^{Y}\sum_{a=1}^{A}\left(J_{ay}^{obs} - J_{ay}\right)^2 \qquad (140)$$

As well as the link model parameters, $q_J$, $q_B$, $v$ and $S_a$, we need to estimate the full set of VPA terminal population parameters $P_{Ay}$ and $P_{aY}$. In addition, we need the relative weights for the series: $\lambda_J$, $\lambda_B$. Note that even if we are particularly interested in

forecasting based on projected effort data, we gain no advantage from weighting the model in favour of the effort index. Incorrect weighting will simply lead to a poorer model, which will produce poorer forecasts. For simplicity, here we assume $\lambda_I = \lambda_B = 1.0$. In a real stock assessment, these relative weights might be the subject of much discussion.

We now fit the model using a two level iterative process. At the outer level, the population model is fitted in the usual way, by using a non-linear numerical optimiser altering the terminal population sizes to minimise the least squares. At the inner level, the link models can be estimated using linear least-squares techniques in one iteration.

**Macro 10.2 This Visual Basic macro solves the VPA equation for $\log_e F_a$ using the Newton-Raphson method and parameters $M_a$, catch and $P_a$. The method is inherently less stable than others presented here, so the function includes additional checks. In particular, if the convergence is very slow, the method tries to leap towards the solution by bisection. This avoids problems such as oscillating around the solution.**

```
Function SolFVPAF(M, Ca, Na_1 As Double) As Double
Dim fx, dfx, C, DeltaD, OldDeltaD, Z, F, G, D As Double
        'Estimate initial F from Pope's cohort equation
G = Na_1 - Ca * Exp(M / 2)
If (Na_1 <= 0) Or (G < 0) Then
 SolFVPAF = Log(10)                    'Return very high F – we're catching fish that
aren't there!
Else
 D = Log(Log(Na_1) - Log(G) )
 Do
  F = Exp(D)                           'Current F
  Z = F + M                            'Calculate total mortality
  G = (1 - Exp(-Z))                    'Temp calculation variable
  C = F * Na_1 * G / Z                 'Catch for current F
  fx = Ca – C                          'Calculate the function
  dfx = C * (M * G / Z + F * Exp(-Z) / G)  'And its -derivative
  DeltaD = fx / dfx                    'Calculate the new correction factor
  D = D + DeltaD                       'Add it to LogF
  If DeltaD < 0.00005 Then Exit Do     'Test for accuracy
  If (OldDeltaD - Abs(DeltaD)) < 0.0000001 Then        'Test for convergence
   D = D - DeltaD / 2                  'No covergence, so guess a new value by
                                       bisection
  End If
  OldDeltaD = Abs(DeltaD)
 Loop
 SolFVPAF = D                          'Return solution
End If
End Function
```

**Table 10.10 Population estimates for the least squares model that uses the survey, biomass and effort indices. The table encapsulates the population model by forward and back-calculation of population sizes based on the catches and 'terminal' populations (shaded cells). Note that the age 10 population sizes are used as the parameters in this model, and the plus group is estimated by forward calculation from the previous year's plus-group population plus new arrivals from the 10 year olds. The shaded cells are the parameters passed to the solver for non-linear minimisation. However, they are not passed directly. A constraint is placed to ensure they never fall below a minimum to cover future catches. If the optimiser were to try parameter values below this amount there would be an error halting the minimisation routine.**

| Age | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 561501 | 345337 | 737407 | 1233835 | 1186411 | 1551036 | 219413 | 579325 | 1152034 | 386663 | 518020 |
| 2 | 252595 | 187756 | 120946 | 237081 | 362551 | 348188 | 411557 | 72348 | 188272 | 306028 | 107001 |
| 3 | 138760 | 146470 | 107819 | 67705 | 130088 | 191258 | 147423 | 161412 | 28023 | 58141 | 93519 |
| 4 | 77549 | 81545 | 91182 | 66221 | 41515 | 68455 | 79064 | 66097 | 66273 | 11797 | 16164 |
| 5 | 42983 | 50764 | 50727 | 61173 | 43668 | 20940 | 27733 | 35137 | 26938 | 24016 | 2832 |
| 6 | 24017 | 30379 | 34569 | 34816 | 37783 | 24244 | 8642 | 12442 | 13834 | 10643 | 5973 |
| 7 | 9807 | 17194 | 21081 | 23784 | 24539 | 21843 | 10872 | 3653 | 4686 | 5264 | 3044 |
| 8 | 3780 | 6993 | 12450 | 14584 | 16150 | 12313 | 7433 | 4498 | 1550 | 1977 | 1303 |
| 9 | 1632 | 2776 | 4915 | 8632 | 9955 | 9002 | 5817 | 2775 | 1900 | 657 | 561 |
| 10 | 1022 | 1177 | 1843 | 3490 | 6137 | 5650 | 4148 | 1639 | 1071 | 602 | 231 |
| 11 | 381 | 976 | 1435 | 2027 | 3272 | 4789 | 3562 | 2531 | 1523 | 740 | 344 |

The link model parameters form part of the calculations in the spreadsheet, so the optimiser never sees them. In essence, the problem has been collapsed over these parameter dimensions, reducing the search volume for the minimum point.

The parameters fed to the optimiser form part of the population model (Table 10.10). There is a danger that the optimiser will attempt to try parameters that are impossible (even if these values are excluded by the constraints within the optimiser!). Once a function returns an error the optimiser will stop, so we need to catch the errors before they occur. The main problem here is that the optimiser will try terminal population sizes, which do not cover the catches in that year. While the VPA functions (e.g. Macro 10.2) may capture these invalid values, we really need to ensure they never enter the model. This can be done by using "IF()" functions as part of the spreadsheet cell calculation. So, for example, in Excel the terminal population size of Age 1 1994 in Table 10.10 could consist of:

```
=IF(P23<N5*EXP($K5/2),N5*EXP($K5/2),P23)
```

where P23 is the cell containing the parameter set by Solver, N5 is the catch and $K5 the natural mortality for this age group. For the age 10 fish, we could have:

```
=IF(R24<(E14+F15*EXP($K14))*EXP($K14/2),(E14+F15*EXP($K14))*EXP($K14/2),R24)
```

where R24 is the parameter, E14 and F15 are the future cohort catches and $K14 the natural mortality for this age group. In both cases we ensure the cohort size will cover all future catches. However, it is important to check that the final estimate returned by the optimiser does not lie on or below the constraint. This would indicate either failure to find the least-squares estimate (restart with the parameter above the constraint) or some deeper problem within the model. Alternatively, and more simply, the optimiser could fit terminal $F$'s, constraining them to be positive. This usually deals with the problem, although we would need an additional constraint for the age 10 fish, as in this model we have included forward calculations for the plus-group. Note, the constraints should also be defined in the optimiser, as this provides important information telling the optimiser the direction to search for the solution. For this reason, the minimum population size functions are best entered in their own cells rather than being calculated in formulas as above.

**Table 10.11 Biomass and biomass indices for fitting the population model. The link model here is linear, so the parameters are calculated by a regression between the $x$ (population model biomass) and $y$ (observed index) variables. The calculations can be carried out using the Equations 67 or by inverting the Hessian matrix (see below), the two methods being equivalent. Notice that the parameter covariance matrix indicates that the correlation between the parameters is very high, so the estimates are inaccurate (The true value for $v$ is 0.4). The results indicate that the $v$ parameter is redundant and could be excluded. However, as the parameters are not going to be used, there purpose being purely to account for variation due to the measurement, it will make little difference in this case.**

| | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Biomass** | 13.319 | 13.312 | 13.375 | 13.506 | 13.593 | 13.767 | 13.631 | 13.627 | 13.674 | 13.543 | 13.434 |
| **Index** | | | | | | | | | | | |
| **Model** | 21.794 | 21.576 | 23.565 | 27.754 | 30.527 | 36.072 | 31.745 | 31.607 | 33.123 | 28.920 | 25.465 |
| **Obs** | 20.207 | 22.361 | 24.055 | 27.812 | 30.705 | 36.337 | 31.857 | 31.643 | 32.447 | 28.506 | 26.219 |
| **Residual** | 2.520 | 0.616 | 0.240 | 0.003 | 0.032 | 0.070 | 0.013 | 0.001 | 0.458 | 0.172 | 0.569 |
| | | | | | | | | | Sums of Squares | | 4.693 |

| Hessian | | Covariance | | | | | |
|---|---|---|---|---|---|---|---|
| 11 | 148.78 | 809.459 | -59.840 | yx1 | 312.15 | $\ln(q_B)$ | -403.11 |
| 148.78 | 2012.56 | -59.840 | 4.424 | yx2 | 4229.19 | $v$ | 31.90 |

Determinant 2.486 Correlation -0.9999

The biomass model used a simple linear regression to account for differences between the observed index and the underlying population biomass (Table 10.11). Again, the link model parameter estimates are obtained by calculation rather than via the non-linear optimiser, although the calculations have become a little more complex. It should become more apparent that bringing more data in the form of indices to bear on the population model produces minimum cost to the fitting process as long as the link models are linear. While for single fits this simplification may be considered useful but not necessary, the use of bootstrapping and other Monte Carlo simulation techniques will soon convince you the value of having short, reliable procedures for estimating parameters.

## 10.4 STRUCTURED LINK MODELS

Using generalised linear models, we can build quite complex link model structures into stock assessment, handling a larger number of parameters than would otherwise be possible. Traditionally, analyses of variables, which might be used in stock assessment are carried out as separate exercises, and only the results are carried forward to the stock assessment. For example, only the year terms of a linear model describing the CPUE of a number of fleets might be used as indices of abundance, the remaining information in the data series being discarded. Although this sequential approach makes analysis easier, it will not be clear how the models interfere with each other and whether information is being discarded which is useful. Explanatory variables may remove variability in the data with which they are correlated, which could be indicators of population changes. It is therefore worth considering carrying out an analysis of the complete model wherever possible. This has largely been avoided simply due to the technical difficulties of fitting models with large numbers of parameters. By carefully structuring models, these problems can often be avoided.

Incorporating linear models suggests an approach to further analysis and simplification. In the biomass link model used previously (Table 10.11), it was found that the $q_B$ and $v$ parameters were too heavily correlated to estimate together. The number of parameters in the linear model therefore could be reduced without significant loss to the model's efficacy. In general, linear regression, analysis of variance and analysis of covariance use analysis of variance tables to make these decisions. We can use similar tables to summarise information about covariates and their power to explain underlying population changes.

In the following example we try to model the fleet structure, testing for differences among vessels using a linear model. It is quite possible to develop much more sophisticated models than that discussed here. In particular, we could use log-linear models to account for changes in catchability alongside population size (McCullagh and Nelder 1983).

Instead of having one fleet, we consider now the case where the fleet is known to be divided in two, a predominantly inshore fleet of small boats, and an offshore fleet of industrial vessels. We wish to know what different effects these fleets have on the stocks. The individual catches and effort of the fleets are available. We can extend the model of fishing effort above to allow for differences between fleets and see if these differences better explain changes in the fishing mortality.

There are essentially five models linking fleets to fishing mortality, based on whether age selectivity is present and whether the fleets have different catchabilities. In general form, the optional link models can be set out as:

$$\begin{aligned}
&\ln(E_{ay}) = \ln(F_{ay}) - \ln(S_1) && 1 \\
&\ln(E_{ay}) = \ln(F_{ay}) - \ln(S_1) - \ln(S_2) && 1+G \\
&\ln(E_{ay}) = \ln(F_{ay}) - \ln(S_{1a}) && 1+A \\
&\ln(E_{ay}) = \ln(F_{ay}) - \ln(S_{1a}) - \ln(S_2) && 1+A+G \\
&\ln(E_{ay}) = \ln(F_{ay}) - \ln(S_{1a}) - \ln(S_{2a}) && 1+A*G
\end{aligned} \tag{141}$$

where subscript $2$ refers to the parameter measuring differences between the two fleets, and subscript $a$ refers to parameters measuring catchability by age. Hence, the first two models do not differentiate catchabilities between ages, whereas the first and third models do not differentiate between fleets. The fourth model allows the fleets to have different catchabilities, but assumes that the selectivity is proportionally the same. The fifth model allows different catchabilities for both fleets as well as ages. The terms 1, $A$ and $G$ refer to the constant, age and fleet effects representing the models in standard generalised linear model (GLM) form. In GLMs, $S_{1a}$ and $S_{2b}$ could be formulated as linear predictors for the catchabilities in a multiplicative model. We would need to implement an iterative weighted least-squares method to allow alternative likelihoods besides the log-normal. In this case however, we can find the least-squares estimates by calculation as the models are assumed log-normal.

By fitting the whole model with each different link model and recording the sum of squares, we can build up an ANOVA table (Table 10.12). The ANOVA table tests how much worse each model does compared to the full model where parameters are fitted to allow for age and fleet differences. It is useful, although not always practical, if the full model, including the population model, is fitted for each link model to generate the sum of squares, as parameters in the link model may be just as well explained as changes in the population size. If it is found that the population model parameters change significantly as the link model is changed, but the sum of squares does not, then there is evidence of conflicting hypotheses, viz. either there are changes in the observations or changes in the population. Without other evidence, the precautionary approach requires assuming the worst hypothesis, even if it requires more parameters. Otherwise, the model with the smallest number of parameters should be chosen as the best model.

**Table 10.12 ANOVA for the fleet link model. The sums of squares are shown for models with increasing numbers of parameters. All models are compared to the fully parameterised model as we would wish to test which terms we can safely remove as they do not explain significant amounts of the variation. The full model is used to estimate the error sums of squares. We can calculate the F statistic as the ratio between the mean square of each model and the error. Those models which show very small F-statistics are equivalent to the full model, and of this group the "worst case" model with the smallest number of parameters should be chosen. In this case, the $S_{1a}$ model is almost equivalent to the full model, indicating that there are no significant differences between fleets. However, as soon as we assume that selectivity does not change between ages ($S_1$ , $S_1$+$S_2$) the model gets significantly worse. Note the approximate F-statistic here may not be distributed as the F-statistic in statistical tables unless the errors are truly normally distributed. However, it can still be used for guidance.**

| Model | SS | Change | df | MS | F Statistic |
|---|---|---|---|---|---|
| $S_1$ | 30.171 | 7.729 | 21 | 0.368 | 5.379 |
| $S_1$+$S_2$ | 30.164 | 7.722 | 20 | 0.386 | 5.643 |
| $S_{1a}$ | 22.722 | 0.279 | 11 | 0.025 | 0.371 |
| $S_{1a}$+$S_2$ | 22.721 | 0.279 | 10 | 0.028 | 0.407 |
| $S_{1a}$+$S_{2a}$ (Error) | 22.442 | | 328 | 0.068 | |

The link models not including an age effect on selectivity showed a significant decline in their ability to explain variation in the data (Table 10.12). Otherwise, there appeared no significant differences between the fleets, so that the fleets can be considered equivalent. This of course does not mean that the catchabilities of the fleets were the same (in fact in the simulation they are not), but that any differences are insignificant compared to other sources of error, and therefore the age selectivity is probably best estimated by combining fleets.

Using ANOVA techniques with these types of non-linear models is potentially dangerous if the statistics are taken too literally. Even if errors are normally distributed, we might expect structural errors to be more severe where linearity cannot be assumed. Nevertheless, calculating statistics based on measures of goodness-of-fit is still very useful in summarising the value of parameters and whole sub-models in explaining variation in the observations even if strict hypothesis testing cannot be reliably conducted.

## 10.5 CROSSLINKED MODELS

It may often be the case that several sets of distinct data will have implications on the same parameters. For example, total catch age composition may be available from commercial sources, as well as more detailed sampled data, perhaps from an observer programme. It is often of interest to link the parameters to both sources of data simultaneously to obtain the best estimates possible.

The problem with separate models linking to parameters of interest is that the data may be in quite different forms. If this is the case, we firstly have to identify some common model, which can be used to develop the links. Likelihood is a useful concept in sorting these issues out. The common ground in likelihood is probability, so all data are compatible across likelihood models, and log-likelihoods can be added. This forms the basis for summing weighted sums-of-squares.

When combining sums-of-squares, it helps to be aware of the underlying likelihood models to ensure we make the correct sum. Broadly, this can be done by converting different data series so that their $x$-variables are compatible, and so all data can be written in a single matrix form. Although you may not actually write out the matrix, you ideally should be clear on how it should be done, as these calculations will form the basis of the data conversion to make it compatible. Often the best way to approach this problem is to consider the original raw data from which the data you have are derived. The raw data themselves may not be available, nevertheless you should be aware of the common fundamental data units (catch per haul, box of commercial groups, vessel landings etc.) from which several data have been derived.

In the following example, a more realistic data set and analysis is developed. The population model and survey data remain the same as used in the above analyses, however we add data taken from a detailed observer survey of commercial vessels which was designed to estimate the impact of new gear technology.

The observer survey was carried out in the same month of 1993 and 1994 and took detailed records of the catch-at-age as well as the gear on board the vessel. The survey was designed to cover vessels with and without two improvements in gear (GPS and monofilament nets) to estimate potential changes in catchability. Under normal circumstances, we would use linear models to estimate the relative change in CPUE due to the different gear use. This would estimate the relative fishing powers, which would be used as fixed adjustments in the stock assessment. However, by doing the analyses sequentially, we would automatically be assuming that all the observed correlation between different gear use and catch rates can be assumed to be due to the gear, not changes in the underlying population size. If this is incorrect, the analysis will be removing useful information from the data without our being aware of the implications to the stock assessment. For this reason, it is always better to try doing the analysis in a single combined model wherever possible.

In the previous analysis, we included the population model when testing whether particular parameters were useful in explaining variation in the data, so we could reduce the model to the most parsimonious possible. This is the preferred method, but it can be very time consuming when not using specialist software. Often this approach is unnecessary for choosing the parameters that will be needed. In this case, a separate linear model analysis on the catch rates should be adequate to identify which parameters are correlated as long as we remove the effective population size for each age group in each year. This can be done by fitting these effects as a minimum model in generalised linear model analysis. Specialist software can then be used to test alternative models, in particular whether factors interact.

Interaction effects are important, and occur where two independent variables together produce a different effect than simply the sum of their independent effects. For example, GPS may have a disproportionately larger effect on vessels also

possessing the improved gear design than on those that do not. Significant interaction effects will lead to a large increase in the number of parameters required by the linear model, as interactions are multiplicative. For example, the number of parameters required to estimate the effect of GPS which does not interact with selectivity would be 12, whereas a significant effect would require 22 parameters, enough to fit two separate selectivities with and without GPS.

While these analyses can be carried out in spreadsheets, interaction effects between discrete factors (such as fleet and gear types) require large numbers of dummy variables to be generated for the different models. This is very time consuming in spreadsheets, whereas specialist statistical software handles these effects automatically. As long as potential effects from population changes can be accounted for, this approach may be preferred in choosing the final model which should be fitted, or at least reducing the number of models to be tested.

In this example, we assume that no significant interaction effects were found between gears and fleets, and gears and selectivity, but that each fleet was found to take a significantly different age composition. The model to be fitted has terms for GPS, monofilament and selectivity by fleet, i.e. 24 parameters. So for a particular survey observation, $i$, the expected catch-at-age can be described by:

$$\begin{aligned} \ln(q_{ia}) &= GPS + Mono + \ln(S_{ga}) \\ C_{ia} &= q_{ia}\tilde{P}_a E_i \end{aligned} \qquad (142)$$

where the GPS and Mono terms are present when those gear were used on the observed vessel, and $g$ indicates the fleet to which the vessel belongs. Because we use logarithms of the data, we assume that the errors are normally distributed and that the model is multiplicative. However, in a few instances catches were zero. To avoid problems with this, we added a constant to catch data.

We also have a time series of effort data, and the proportion of GPS and monofilament in the fleets since 1984. We wish to estimate simultaneously the GPS, Gear and fleet selectivity parameters for both the observer vessel survey and total effort.

In simulations, it is easy to assume some level of convenience in what data the scientist possesses. For instance, in the previous example we happen to have catches separated by fleet. In practice, data, or the lack of it, is usually the main problem in the analysis. In this scenario, it is assumed we neither have catches separated by fleet nor gear type, only age. However, if we at least know the proportional gear use, we can still calculate the expected fishing mortality in each year as the weighted average of the fleet combined.

$$\begin{aligned} \ln(q_{ay}) &= w_{gps}GPS + w_{gear}Gear + w_{fleet}\ln(S_{1a}) + (1 - w_{fleet})\ln(S_{2a}) \\ \ln(F_{ay}) &= \ln(q_{ay}) + \ln(E_y) \end{aligned} \qquad (143)$$

where the weights, $w$, are the proportion of the fleets in each category. Notice that although the linear model is the same as Equation 142, the catchability is linked to

the fishing mortality rather than population size. Equation 142 can be fitted as long as we have the weights, total effort and fishing mortality.

The two catchabilities in Equations 142 and 143 will be equivalent as long as the survey observation lasts a short time. Although any change in population size during the survey observation will introduce a structural error between the two models, this difference is unlikely to be significant if the time period is small. Both models are only approximations to reality. For example, the fishing mortality model assumes a constant exploitation rate during the period it applies and an instantaneous reaction from catch rates to removals. The difference model, relating average stock size to catch rates over a fixed period assumes a delay between removals and catch rate change, and the change is a step function. Neither is strictly correct.

### 10.5.1 Fitting the Model

The fitting procedure for Equations 142 and 143 is more difficult than those previously discussed. One option is to use a non-linear standard fitting routine, finding the least squares solution to fitting the observed and expected mean log CPUE for the survey data (by manipulating Equation 142) and mean log total yearly effort (defined by manipulating Equation 143). Although this is fine for the survey data, it produces an incorrect result for the effort model. This is because the least squares solution for effort model is incorrect as we have not considered all combinations of the vessel characteristics from which observed mean fishing mortality has been derived. We first assume gears are distributed among categories proportionally. So if 20% of all vessels possess GPS, also 20% of the vessels in fleet group 2 using monofilament have GPS. Under these circumstances, the mean log fishing mortality of age $a$ fish is:

$$\begin{aligned}\ln\left(F_{ay}\right) = \ln\left(E_y\right) &+ w_{gps}w_{gear}w_{fleet}\,\eta_{gps,gear,1a} + \left(1-w_{gps}\right)w_{gear}w_{fleet}\,\eta_{gear,1a} \\ &+ w_{gps}\left(1-w_{gear}\right)w_{fleet}\,\eta_{gps,1a} + \left(1-w_{gps}\right)\left(1-w_{gear}\right)w_{fleet}\,\eta_{1a} \\ &+ w_{gps}w_{gear}\left(1-w_{fleet}\right)\eta_{gps,gear,2a} + \left(1-w_{gps}\right)w_{gear}\left(1-w_{fleet}\right)\eta_{gear,2a} \\ &+ w_{gps}\left(1-w_{gear}\right)\left(1-w_{fleet}\right)\eta_{gps,2a} + \left(1-w_{gps}\right)\left(1-w_{gear}\right)\left(1-w_{fleet}\right)\eta_{2a}\end{aligned} \tag{144}$$

where $\eta_{gps,gear,1a}$ indicates the linear predictor with terms GPS, Gear and fleet-age ($S_{1a}$) as in Equation 143. Adding over the terms, the mean is exactly the same as that in Equation 143. But the contribution of the individual fleet categories to the sum-of-squares is different:

$$\eta_{ai}^{obs} = \ln\left(F_{ai}^{obs}\right) - \ln\left(E_i^{obs}\right)$$

$$\begin{aligned}Minimise\quad & w_{gps}w_{gear}w_{fleet}\left(\eta_{ai}^{obs}-\eta_{gps,gear,1a}\right)^2 + \left(1-w_{gps}\right)w_{gear}w_{fleet}\left(\eta_{ai}^{obs}-\eta_{gear,1a}\right)^2 \\ &+ w_{gps}\left(1-w_{gear}\right)w_{fleet}\left(\eta_{ai}^{obs}-\eta_{gps,1a}\right)^2 + \left(1-w_{gps}\right)\left(1-w_{gear}\right)w_{fleet}\left(\eta_{ai}^{obs}-\eta_{1a}\right)^2 \\ &+ w_{gps}w_{gear}\left(1-w_{fleet}\right)\left(\eta_{ai}^{obs}-\eta_{gps,gear,2a}\right)^2 + \left(1-w_{gps}\right)w_{gear}\left(1-w_{fleet}\right)\left(\eta_{ai}^{obs}-\eta_{gear,2a}\right)^2 \\ &+ w_{gps}\left(1-w_{gear}\right)\left(1-w_{fleet}\right)\left(\eta_{ai}^{obs}-\eta_{gps,2a}\right)^2 + \left(1-w_{gps}\right)\left(1-w_{gear}\right)\left(1-w_{fleet}\right)\left(\eta_{ai}^{obs}-\eta_{2a}\right)^2\end{aligned} \tag{145}$$

where $\eta$ is the model linear predictor, e.g. $\eta_{gps,gear,2a} = GPS + Gear + \ln(S_{2a})$

Hence Equations 143 and 144 only give the least-squares estimate of the log fishing mortality per unit effort for $\eta^{mod}$ as if it were a single parameter, but not the individual parameters that make up the linear predictor. Correct fitting for the individual parameters requires consideration of all combinations of attributes parameterised in the model. The weights refer to the inverse variance of the estimated catch rate within each category, rather than a contribution to a mean value. We need to calculate correctly the sum-of-squares so that we can combine with information from other sources, and for this, the full weighted combinations are necessary.

This illustrates an important point. Often statistics are taught covering simple procedures where underlying assumptions are implicit. In real-world problems of fisheries, some assumptions may well turn out to be incorrect. It is therefore always worthwhile returning to the basic procedures and checking which simplifying assumptions may be used. Although not directly observed, the fundamental data are the individual vessel catches per unit effort ($y$-variable) and the gear they possess ($x$-variables). This is essentially the data we have from the scientific vessel survey. From this simple point, we need to develop a model of how the observed variables, the annual fishing mortality per age per unit effort, would arise. To do this, we could gather all individual observations into groups with the $x$-variable combinations (i.e. gear), and calculate the average $y$-variable and the weighting factor for each group. This is essentially, Equation 145. What you would not do is add up the catch rates of all the vessels with each gear type into groups, as vessels with more than one gear type would appear in more than one group. This is what we would be doing if we used Equation 143 as the basis for an estimator.

The GPS, Gear (monofilament) and fleet selectivities are discrete factors and must be represented in fitting the model as dummy variables. Dummy variables take on a value of one when its parameter applies and zero when it does not apply (

Table 10.13). The $x$-variables, can, as in this case, consist solely of binary values. Analysis of variance and covariance are based on this type of model. Once we have generated a full data matrix of all fleet-gear combinations in each year, joined to the same format matrix for the survey observations, we can multiply the data matrix ($n$ observations on $m$ $x$-variables) by a parameter vector ($m$ estimates) to produce a vector of expected values of $q_{ia}$ (length $n$). We can calculate the sum-of-squares comparing the expected $q_{ia}$ with the observed calculated from the log CPUE and population size for the survey, and the expected $q_{ia}$ with the observed calculated from the log fishing mortality and total effort. We add this sum-of-squares to the sums-of-squares from the scientific resource survey and can pass this total sum to an optimiser to minimise with respect to the terminal population sizes and the linear model. If you do this, despite having 45 parameters and a data matrix length of over 1000 observations, the optimiser should be able to find the minimum reasonably quickly, 5-10 minutes on a fast desktop computer. Optimisers in general will do reasonably well, as they often assume linearity to find trial solutions (as in the Hessian matrix), so the 24 parameters belonging to the linear model do not prove too great an obstacle. Even if you try to improve on this approach, it may be worthwhile to estimate values this way initially. As you set up more complicated but more

efficient approaches, you can then ensure the method is correct as the resulting estimates should be very close if not exactly the same.

**Table 10.13 Example dummy for two observations. One of a vessel of fleet type 1 with GPS, but not the improved gear design and another of a vessel of fleet type 2 with GPS and improved gear. The age class of the catch is a discrete factor variable with 11 levels. Unlike the GPS and Gear terms, these are mutually exclusive, so a vessel can either be of type 1 or 2, but not both and the catch can be of only one age. The data set possesses catch and effort covariates. Catch will vary with age categories, but effort will remain constant across a single survey observation. The number of columns, GPS to Age (S2a) 11 is the same as the number of parameters required by the model.**

| | | | Age (S1a) | | | | | | | | | | | Age (S2a) | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year | GPS | Gear | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
| 1993 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1993 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |

There are a number of reasons why this straightforward approach may not be desirable:

- **Building the matrix:** The number of factors and matrix structure may have to be generated. Given the size of the matrix, this may require a great deal of typing and copying values and may make it easy to introduce mistakes. In this case, we can generate the sums-of-squares more directly than using dummy variables because the weights are multiplicative. If there were different weights for each gear-catch combination category, we may still have to generate the full matrix.

- **Computer memory inadequate:** The matrix length for the total effort model would account for 2 fleets, 2 gears, 2 GPS, 11 age and 11 year categories, producing a grand total of 968 rows in the matrix (to estimate only 11 effort values!). For more interaction terms, the number of rows would be much larger

than this and easily overflow memory on smaller computers. However, it is relatively easy to produce the Hessian (information) matrix, which has the same length as the number of parameters and holds all the information necessary for finding the least squares solution in the linear model.

- **Speed of calculation:** This is probably the most important issue. While 10 minutes computing time for one fit seems short, it very soon adds up. A proper stock assessment will always need to assess how robust the results are to changes in assumptions, and therefore a number of fits are required to test sensitivity. Even after you are satisfied with the model, the chances are that you will wish to generate bootstrap estimates for confidence intervals and other statistics. If you require 1000 bootstrap estimates, each taking 10 minutes, it will take about 7 days to get an adequate number. Since Murphy's Law invariably means you find you have forgotten to divide some critical value by 2 after completing 500 bootstraps, reducing this time to a minimum is important. This can be done both by reducing the size of the matrix and solving the linear model directly, by-passing the non-linear optimising routine.

#### *10.5.1.1 Using Weights*

Using weights is often the simplest way to reduce the size of data sets without losing pertinent information. All data records which possess the same $x$-variable values can be combined in this way. The use of weights is underpinned by the assumption of normal errors, and is strictly the inverse variance of the $y$-variable. However, the method is more generally valid as long as the weights represent the relative changes in variance of the $y$-variable.

In any case where raw data records are combined, weights should be considered to account for changes in variance. For the observer data, the original form of data was daily records. These were combined into total catch and effort by vessel. If the log-catch on each day is normally distributed, the variances will be additive, so the variance of the total values will be proportional to the number of observations (i.e. the effort) that are combined to make them. If the model and relative variances are correct, the relevant information in the data for estimating least squares can be maintained in a smaller data matrix with totals and weights. However, it is worth confirming the weighting is correct, by examining model residuals, ensuring they show variation consistent with their weights.

#### *10.5.1.2 Solving Linear Sub-Models*

Probably the most robust method for solving linear least-squares problems is Singular Value Decomposition (SVD). SVD will decompose a data matrix into a form that allows a solution to be found to the simultaneous differential equations very rapidly. There are several advantages to this approach.

- The least-squares estimates are more accurate than those obtained from a non-linear optimiser and take less time to solve.

- If only the $y$-variable changes, the least-squares parameter estimates can be found without having to decompose the matrix again. This is very useful in this context, where only the $y$-variable is affected by changes in the population size. If

you are able to construct your models in this form, where the x-variables and weights do not change, SVD offers considerable increases in speed as well as reliability.

#### *10.5.1.3 Using the Linear Information Matrix*

The Hessian matrix in linear regression is often known as the information matrix. It summarises the data with respect to the $x$-variables, and with the $xy$-vector represents the normal equations, which solve the least-squares problem. SVD also works on the information matrix as well as the data matrix. The information matrix is a square matrix with length of sides equal to the number of parameters. Calculation of the information matrix where it is relatively fast, or only has to be carried out once, may reduce both memory use and calculation time in finding least-squares solutions. However, if the solution is nearly singular (i.e. parameters aliased or too heavily correlated), using the information matrix may increase instability of the results.

Each cell in the linear information matrix is the sum of the products of pair of $x$-variables as identified by the row, $j$, and column, $k$, and each row in the $xy$-vector is the sum of the product of the $j^{th}$ $x$-variable times the $y$-variable.

$$X^T X = \begin{Bmatrix} a_{11} & \cdots & a_{1m} \\ \vdots & \ddots & \vdots \\ a_{m1} & \cdots & a_{mm} \end{Bmatrix}$$

$$a_{jk} = \sum_{i=1}^{n} x_{ij} x_{ik} \qquad (146)$$

$$X^T Y = \begin{Bmatrix} \sum_{i=1}^{n} x_{i1} y_i \\ \vdots \\ \sum_{i=1}^{n} x_{im} y_i \end{Bmatrix}$$

The $x^2$ variables are making up the diagonal of the information matrix, and the matrix will be symmetric ($a_{kj} = a_{jk}$). To take as an example the observer survey model (Table 10.14), Equation 146 consists of multiples of dummy variables, which indicate whether a vessel possesses a particular gear, or the age group of the catch. So matrix term $a_{11}$ is the number of all observations possessing GPS and $a_{12}$ is the number of all observations possessing both GPS and the new improved gear. An observation is the catch of a particular age group by a vessel of either fleet 1 or fleet 2. Age groups and fleets are mutually exclusive, so most of the cells, such as $a_{34}$ to $a_{3,24}$, are zero. If we had no GPS or Gear effect, which crosses over age-group and fleet, each age-group and fleet combination would be independent and their parameters could be estimated separately – a much easier task.

**Table 10.14 Information matrix of dummy variables from the observer survey. As the GPS and Gear (mono) effects are non-zero across all other parameters, these are the effects sticking the matrix together. If they were removed, the matrix could immediately be decomposed into 22 separate matrices of fleet-age group combinations, which would estimate the parameters independently. Notice that on each side of the diagonal, the matrix elements sum to the diagonal.**

| | GPS | Gear | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GPS | 88 | 44 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| Gear | 44 | 66 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| 1 | 4 | 2 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 4 | 2 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 4 | 2 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 4 | 2 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 4 | 2 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 4 | 2 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 7 | 4 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 8 | 4 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 9 | 4 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 10 | 4 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 4 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 | 0 |
| 7 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 | 0 |
| 8 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 | 0 |
| 9 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 | 0 |
| 10 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 | 0 |
| 11 | 4 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8 |

Introducing weights, as we must in the effort model, makes the calculations a little more complicated. For the SVD method, we need to multiply each record (row) of the data matrix by the square root of its weight. This is a little easier to calculate in this case, as the weights are simple multiples of the proportion each gear category occurs in the observations overall (Equation 145). When using SVD to decompose the matrix, weights represent inverse standard deviations rather than variances, so the square roots of the weights are used rather than the original weights themselves. For example, in the effort model $b_{13}$ would be the cell representing age 1 fish caught by a fleet 1 vessel with GPS, irrespective of whether they possess the improved gear or not:

$$b_{13} = \sum_{i=1984}^{1994} \sqrt{w_{gps,i}} \sqrt{w_{fleet,i}} \left( \sqrt{w_{gear,i}} + \sqrt{1 - w_{gear,i}} \right) \tag{147}$$

Similarly the result for the cell representing observations with GPS and the improved gear, irrespective of fleet or age group is:

$$b_{22} \doteq 11 \sum_{i=1984}^{1994} \sqrt{w_{gps,i}} \sqrt{w_{gear,i}} \left( \sqrt{w_{fleet,i}} + \sqrt{1 - w_{fleet,i}} \right) \tag{148}$$

and so on. Notice in this case we have 11 observations within each category as we are summing over age groups. The resulting information matrix (Table 10.15) shows a similar pattern to Table 10.14, with most non-diagonal elements remaining at zero.

The observed $y$-variables are the adjusted log-CPUE. The adjustment is derived from the population model and is a fixed offset when fitting the linear model (i.e. there is no parameter to be fitted to this input). This means either the $x$ or $y$-variables can be adjusted without affecting the error model, but it is much more efficient to apply the adjustment to the $y$-variable. The population size is used for the observer survey model and fishing mortality for the total effort model:

$$y_i^{obs} = \ln(C_{ia}) - \ln(\tilde{P}_a) - \ln(E_i) \tag{149}$$

where $i$= observer data grouping (refers to the GPS-gear-fleet/age combination), and

$$y_i^{obs} = \ln(F_{ia}) - \ln(E_i) \tag{150}$$

where $i$= year.

To create the final information matrix, equivalent cells are added:

$$c_{jk} = \sqrt{\lambda_a}\, a_{jk} + \sqrt{\lambda_b}\, b_{jk} \tag{151}$$

where $\lambda_a$ and $\lambda_b$ are the relative weights given to observer survey and total effort data models respectively. Similarly, equivalent rows are added in the $xy$-vector. This final matrix can be decomposed by SVD to obtain the least-squares estimates.

**Table 10.15 Information matrix of the weighted dummy variables for the total effort and fishing mortality model. The patterns in the matrix are similar to Table 10.14.**

| | GPS | Gear | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GPS | 35.53 | 19.46 | 1.35 | 1.35 | 1.35 | 1.35 | 1.35 | 1.35 | 1.35 | 1.35 | 1.35 | 1.35 | 1.35 | 1.88 | 1.88 | 1.88 | 1.88 | 1.88 | 1.88 | 1.88 | 1.88 | 1.88 | 1.88 | 1.88 |
| Gear | 19.46 | 115.43 | 5.23 | 5.23 | 5.23 | 5.23 | 5.23 | 5.23 | 5.23 | 5.23 | 5.23 | 5.23 | 5.23 | 5.26 | 5.26 | 5.26 | 5.26 | 5.26 | 5.26 | 5.26 | 5.26 | 5.26 | 5.26 | 5.26 |
| 1 | 1.35 | 5.23 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 1.35 | 5.23 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 1.35 | 5.23 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 1.35 | 5.23 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 1.35 | 5.23 | 0 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 1.35 | 5.23 | 0 | 0 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 7 | 1.35 | 5.23 | 0 | 0 | 0 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 8 | 1.35 | 5.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 9 | 1.35 | 5.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 10 | 1.35 | 5.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 1.35 | 5.23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 11.91 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 | 0 | 0 |
| 7 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 | 0 |
| 8 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 | 0 |
| 9 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 | 0 |
| 10 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 | 0 |
| 11 | 1.88 | 5.26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10.65 |

Although the information matrix provides the least-squares estimate for the linear parameters, it does not calculate the sum-of-squares statistic which is needed to estimate the non-linear part of the model. Calculating the sum-of-squares for the observer survey data is simple as the data matrix is small. We can calculate the expected $y$-value for each data record. If we do not have the full matrix for the total effort model, the situation is a little more complicated. To do the calculation we need all the different y-values, which only change with age and year, not gear type, and the separate model y-values derived from the parameter estimates of the different gear and fleet combinations, and the catch age. Hence, the sum-of-squares is Equation 145 summed over year and age group. In both cases, the sum-of-squares need to be multiplied by their respective weights, $\lambda_a$ and $\lambda_b$ before being added to the scientific fish population survey sum-of-squares.

#### *10.5.1.4 Results*

In an Excel spreadsheet, the model takes about half the time to fit using a non-linear solver if the linear component is fitted separately. However, you will need to set up the model in a form, which avoids inefficiencies in the way the spreadsheet is calculated.

We can see how well the model performs by plotting the residuals. The observer survey data indicates some problems with decreasing variation with larger expected values (Figure 10.2). This is often due to taking logarithms of data, where the variance increases less dramatically than expected with the mean. A second problem with logarithms is that they do not cope with zero values. To get around this a

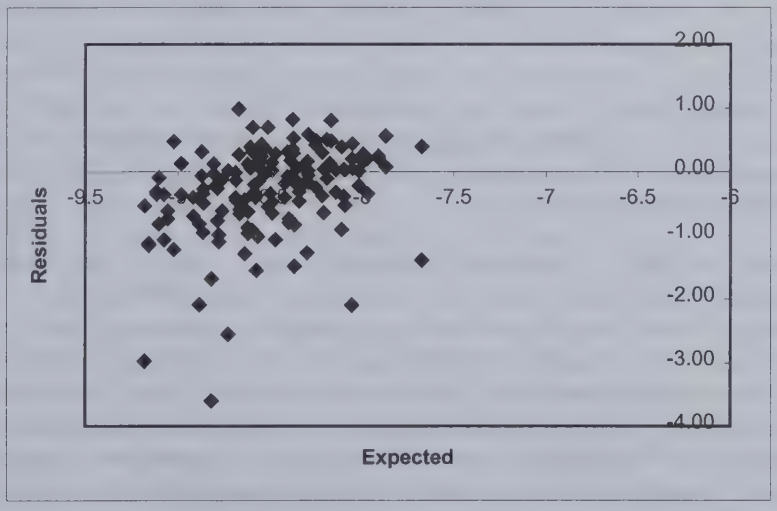


**Figure 10.2 Residuals plotted against expected values for the observer survey model. The residuals suggest a decreasing variance with larger expected values. This suggests that there is room for improvement in the error model.**

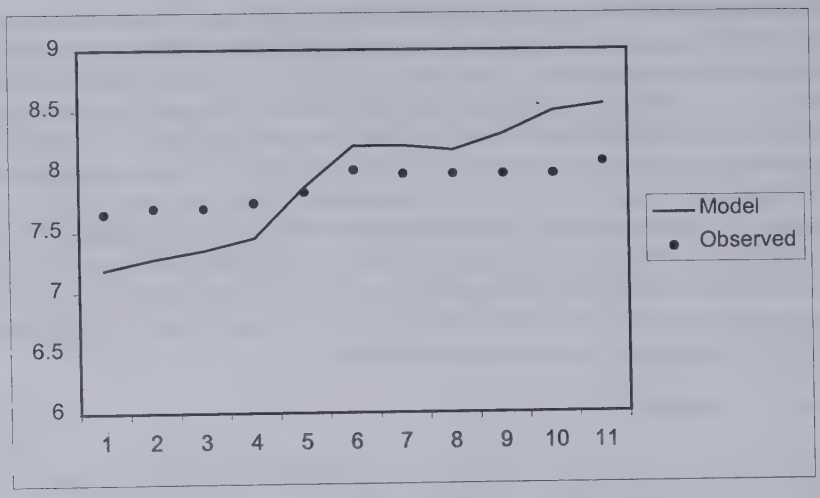


**Figure 10.3 Observed and expected log-effort based on the fitted model. The model exhibits systematic error in the time series. The effort is overestimated in recent years suggesting that catchability is underestimated. This would be of great concern in recommending future effort levels. The systematic trend can be reduced by weighting in favour of the total effort model against the observer survey model, at a cost of a poorer fit to the observer survey. However, if the effort data is poor, it may be felt it is more likely trends like this is due to poor data than the fitting process.**

constant was added to all values before taking logs. The constant cannot be estimated. The current value, 1.0, was chosen to minimise the effect of negative residual outliers. The errors are not so badly modelled that we would reject the results, although there is room for improvement. There are alternative approaches to dealing with errors in generalised linear models, which allow multiplicative models, but use variance functions instead of transforms. The cost is increasing the number of iterations to find a solution.

A common problem in combining separate data sets is that error models are incompatible. The main tool for improving compatibility is to weight data appropriately. Firstly, we might introduce a weighting scheme in the observer survey model to account for the increasing variance for smaller expected CPUE. Secondly, we might increase the weight on the total effort series, forcing the estimated effort to follow the observed effort more closely. In most cases, we would probably only have a vague idea of the relative variance of the two series, so this decision would probably be mostly down to judgement. As the weight for the total effort model is increased, it would be necessary to check whether the effect was primarily on catchability or fishing mortality, and what implication the weighting scheme would have on decision-making.

### 10.5.2 Indicators and Reference Points

Although we may have estimated the current population sizes and catchability parameters as well as possible, we still need to interpret the results and provide a

summary of the stock status. We achieve this by calculating some indicators of stock status, together with their reference points.

Reference points are required for the interpretation of indicators. For example, an indicator might be the spawning stock biomass (SSB). However, if the SSB was reported as 120 000 tonnes, without a reference point it is not possible to know whether this indicates an overfished stock.

The unexploited spawners per recruit can be calculated by using the spawning ratio in each age group and natural mortality. For this, we need an estimate of the proportion surviving to each age in the unexploited stock:

$$\mathrm{P}_a^u = e^{-\sum_{t=1}^{a-1} Z_t} \tag{152}$$

or recursively as:

$$\mathrm{P}_{a+1} = \mathrm{P}_a e^{-Z_a} \tag{153}$$

where $Z_a$ is the total mortality at age and is equivalent to natural mortality in the unexploited stock:

$$\mathrm{P}_{a+1}^u = \mathrm{P}_a^u e^{-M_a} \tag{154}$$

If spawning, for example, occurs during the year, rather than on the 1st January, the estimates can be adjusted to represent the survivors to this time:

$$\mathrm{P}_{a+1} = \mathrm{P}_a e^{-((1-\alpha)Z_a + \alpha Z_{a+1})} \tag{155}$$

where $\alpha$ is the proportion of the year which passes before spawning occurs. The expected survivors gives us a range of per recruit reference points and indicators. We can sum the product of survivors multiplied by some attribute such as weight of the fish (biomass) or proportion mature (spawners) or fecundity (eggs):

$$I_{pr} = \sum_{a=1}^{\infty} v_a \mathrm{P}_a = \sum_{a=1}^{A-1} v_a \mathrm{P}_a + \frac{v_A \mathrm{P}_A}{1 - e^{-Z_A}} \tag{156}$$

where $v_a$ is the average weight, proportion mature, egg production etc. at age $a$, and $A$ is the plus group of the population. A reference point is any value that $I_{pr}$ can become and which can usefully be compared to the current value. Zero is always an implicit reference point, but by-itself is of little value. To scale $I_{pr}$ we also need to know its maximum value, which will occur when there is no fishing (Equation 154). The ratio of the current indicator value to its maximum gives a dimensionless indicator as a percentage of the stock status with respect the attribute $v_a$.

Using Equation 156, the total spawning stock biomass (SSB) can be calculated and compared with an unexploited stock. In this case, however, we need to include some model of recruitment. Again, we chose a simple model, the arithmetic mean of the

observed recruitment series (although the median value could just as easily have be chosen if the recruitment estimates were very widely dispersed).

$$B_\infty = R_0\left(\sum_{a=1}^{A-1} w_a s_a \mathrm{P}_a^u + \frac{w_A s_A \mathrm{P}_A^u}{1-e^{-Z_A}}\right) \tag{157}$$

where $w_a$ is the weight at age, $s_A$ is the proportion spawning at age and $R_0$ is the mean number of recruits. The current SSB is the current estimates of the population size at age multiplied by their average weight.

$$B_t = \sum_{a=1}^{A} w_a s_a P_a \tag{158}$$

Again the ratio $B_t/B_\infty$ is a useful reference point to measure how far below the unexploited SSB the current population is. Note that it is possible, although unlikely, that the current SSB lies above the unexploited level if the exploitation rate is low and there have been a series of recruitments greater than the average in the recent past.

The biomass level is a snap-shot of the current population size. These snap shots can be taken forward in time as long as any external variables, such as effort and recruitment are known. The projections use the same models as described in the estimation procedure with the best estimates from the least-squares fit. The recruitment in both years is assumed to be the mean of the estimated recruitment series, and the effort and fleet is assumed to remain constant with the exception that the proportion of vessels using GPS increases to around 75% from 55%. This proportional change in GPS use is applied to the 1994 fishing mortality which otherwise remains the same.

Reference points have an important role in minimising the effect of unknown factors which otherwise have a dramatic effect on uncertainty. References to the unexploited stock primarily aim to remove the effect of natural mortality. Varying natural mortality over the whole life history mostly rescales the stock size rather than affects the fitted model. Although small changes can have very large effects, by using reference points we largely eliminate them. However, if natural mortality changes within the life history, while reference points help reduce these effects, they do not eliminate them altogether and this source of uncertainty may need to be addressed more directly.

## 10.6 BOOTSTRAPPING BASED ON MONTE CARLO SIMULATIONS

Bootstrapping is a very powerful technique to explore the effect of random errors on the estimation technique. Bootstrapping is also used in medium-term simulations, Section 9.4, and for calculation of confidence intervals on parameters and reference points, Section 7.3. Bootstrapping is based on Monte Carlo techniques used to generate simulated datasets with known error properties. To demonstrate the approach, we use the analysis described above, including the observer survey and total effort link models.

The aim of bootstrapping methods is to simulate data sets with errors to test how well the estimation procedure works. The data sets should be simulated, as nearly as possible, to exactly the same form as the original data in the fit. Least-squares estimates produce fitted values (expected values) and residuals. By randomising or simulating the residuals, we can produce new imaginary data sets to which the estimation procedure can be applied.

Although we do not do it here, the procedure can easily be extended to deal with all sources of uncertainty:

**Fixed Parameters**: Some parameters are given as fixed known values when in reality they are poorly known, such as natural mortality. While use of reference points deals with natural mortality as a scaling factor, the other effects of the particular choice of value are unknown. The simplest way to explore this issue is to simulate the error in the parameter and see how it affects the final estimated statistics.

**Structural Errors**: The fitted model is often called the estimation model. However, biologists may possess alternative more complex models describing the population dynamics in a way that they feel is closer to reality. While the type of data available may prevent fitting these models, they may still be used to simulate data. This allows the analyst to assess the effect of possible structural errors in the estimation model.

**Management Controls**: It is also possible to simulate the whole management process. This procedure requires not only simulated data, but also management controls, which are applied when particular results are returned from the stock assessment. By projecting the fishery forward, we can see how well the rules perform when knowledge is less than perfect. This should be the ultimate arbiter on both the assessment advice and management controls.

**We only consider estimating the variation of the fitted parameters, the basic Monte Carlo simulation. Extensions to this would allow all the types of simulations above. However, the principles remain the same (see Figure 10.4). The simulations provide a frequency framework to describing uncertainty and its implications to management.**

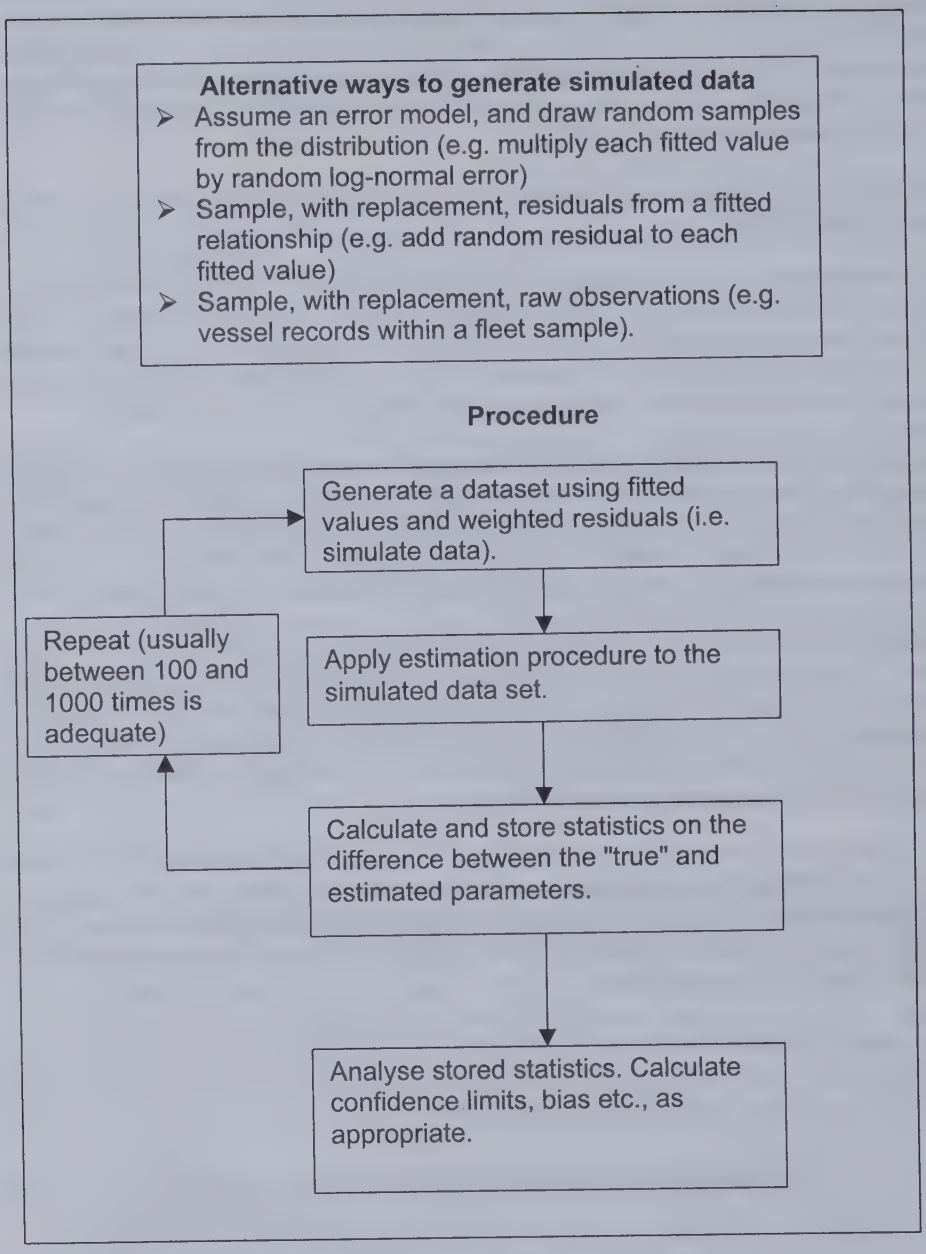
Alternative ways to generate simulated data
Assume an error model, and draw random samples from the distribution (e.g. multiply each fitted value by random log-normal error)
Sample, with replacement, residuals from a fitted relationship (e.g. add random residual to each fitted value)
Sample, with replacement, raw observations (e.g. vessel records within a fleet sample).
Procedure
Generate a dataset using fitted values and weighted residuals (i.e. simulate data).
Apply estimation procedure to the simulated data set.
Calculate and store statistics on the difference between the "true" and estimated parameters.
Repeat (usually between 100 and 1000 times is adequate)
Analyse stored statistics. Calculate confidence limits, bias etc., as appropriate.

**Figure 10.4 The general bootstrap procedure for investigating the performance of estimation methods. Although all procedures are broadly the same, they may be based on different sources for the random variables. The bootstrap approach can be used to estimate the degree of bias, the parameter confidence intervals or any other issue related to uncertainty.**

### 10.6.1 Specifying Errors

We are simulating the estimation model only. The original data in the model were the scientific survey population indices, the observer vessel survey and the total effort. Catches were assumed to be known exactly, so they have no error.

Errors for the population index and observer survey can be derived in the same way. The original data is decomposed into the least-squares fitted value for the data point, and the residual, the difference between the observed and fitted value. It is the sum-of-squares of the residuals that the model fitting process aims to minimise. These residuals can be randomly sampled-with-replacement and added to the fitted value to create a new data set. For the population survey data this is straightforward. For the observer survey we can only simulate the transformed variable ($\mathrm{Ln}(Y_i+1)$). This means that some simulated values cannot be translated back to real catches (i.e. when the simulated value is less than one), which is a direct artefact of the presence of zeros in the data. Although not entirely satisfactory, it is unlikely that the few values for which this is a problem will influence the results of the simulation too greatly.

Although we can generate fitted values and residuals for the log total effort series, there are only 11 data points. A fundamental assumption of bootstrapping is that each set of random residuals and hence simulated data, is random and independent. While for non-parametric bootstraps this is always violated, the dependence effect is small for large data sets. In these circumstances, the robustness of not having to specify any particular error distribution more than out-weighs this cost in accuracy. For small data sets, the use of residuals is moot. For these the correlation between simulated data sets would probably mean the variation in fitted parameters is biased or underestimated. Under these circumstances, it is better to simulate the error from a parametric probability distribution, but make the simulated error similar to the observed residuals. Hence, for the current analysis we could simulate normal errors based on the standard deviation of the residuals. These could be added to the fitted effort values in exactly the same way to create new simulated effort data, except that we would convert residuals with a clear pattern (Figure 10.3) to a series with random errors and no pattern.

So far we have assumed that the errors are well-behaved. That is the errors within each model are independent identically distributed random variables. In many cases they are not, but we would still like to construct an error simulation. If weights vary between data records the method is straightforward. The weights are the inverse (relative) variance, so we can standardise all the residuals by multiplying them by the square root of the weight (often called the Pearson residual). These standardised residuals can be sampled and divided by the appropriate weight before adding to the fitted value.

Suspected systematic error (e.g. Figure 10.3) is more difficult to deal with. Effectively we need to propose a second model. Systematic errors often occur in time series and may take the form of autocorrelation or trends. If autocorrelated, you may wish to weight the model in line with the level of autocorrelation as the series effectively contains less information than might at first appear. This takes the form of weighting the series (in addition to other weights) by a factor related to the autocorrelation. This is not necessary if the only data you have is autocorrelated and you plan only to

estimate parameter errors through a bootstrap, which is taking account of autocorrelation. However, for relative weights between different data sources this may be a good basis for $\lambda$. Autocorrelation can be simulated, but we need to define how it has arisen. In most cases, an autoregressive model would probably suffice.

Trends in residuals can be accounted for by linear regression, but a better approach is probably differencing the data. Single differencing removes linear trends, differencing twice removes quadratic trends and so on with higher order polynomials. If, after differencing and applying weights so that the series is stationary, the errors are autocorrelated, some model for the autocorrelation can also be fitted. This then would form the basis for simulation, developing autocorrelated errors from the model and applying a reverse of the differencing to generate random errors which possess the same systematic patterns as those observed from the model fit. If you are familiar with time series analysis, you will by now have noticed a description of Box-Jenkins ARIMA models (Chatfield 1984, Diggle 1990).

The ARIMA approach should only be carried out for the simulation if you have been unable to remove the systematic error in the original analysis. Autocorrelations and residual trends are not desirable, and should, if you simulate the error correctly, increase the uncertainty in the results. However, if they are present, they need to be represented in some way in the simulation so that the full uncertainty is represented and the results are not viewed with misplaced optimism. If, on completing the simulations, the stock status and recommendations are, overall, not affected by this source of error, recommendations can still be made despite misgivings about the final form of the model.

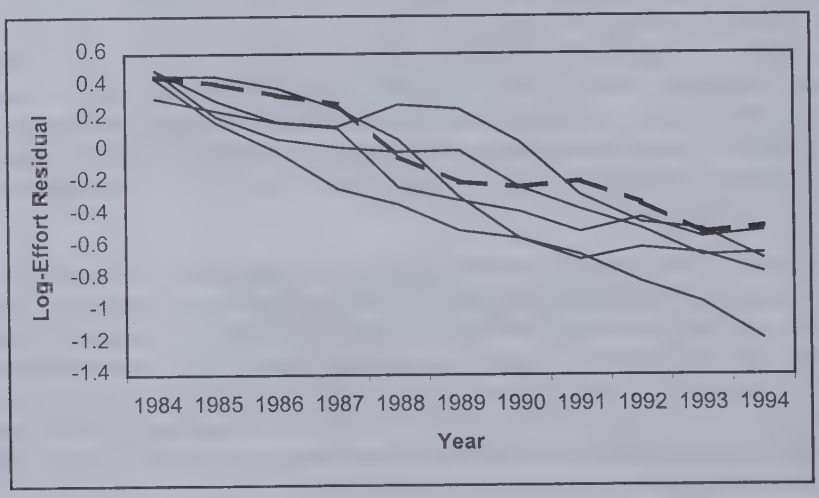


**Figure 10.5 Original (— —) and simulated (——) residuals for the log-total effort model. The systematic trend is maintained, but the simulated residuals show random divergence from the original systematic trend. The simulated data represent data that we could have obtained if the underlying model is correct, but that the errors are influenced by time series effects that are unaccounted for.**

So, we certainly have misgivings about the total effort model (Figure 10.35). Assuming that we are unable to fix the problem in the original model in the time available, how should we represent it in the simulation. We firstly obtain the residuals in the normal way. They have a negative slope. The first differences have no slope, and no obvious autocorrelation (the time series is short, however). If we assume the slope is systematic as opposed to random, we can use the fixed mean of the differences to represent the trend. So, we simulate the error as a normal variate with mean and standard deviation equal to the mean and standard deviation of the differences. It should be emphasised this does not solve the problem in sense that the unknown bias continues to be present, but at least you can simulate realistic data sets that include the residual trend.

Once the simulated data are obtained the full model is fitted to those data in exactly the same way as in the original least-squares model to obtain simulated parameter estimates, indicators and reference points. These can be stored in a table for analysis.

### 10.6.2 Results

Overall the fit and subsequent bootstrap estimates relate well to the underlying "true values" used to simulate the original data (Table 10.15). In particular, it is worth checking the parameter bias, as these can be very large in some cases so that the true value lies outside the confidence intervals. Bias while present, is not so large as to invalidate the results and broadly they are correct. The stock is overfished and the situation will only get worse unless urgent action is taken.

The exception, and a very important one, is the recruitment in 1994. Despite the simulation the variation estimated in this parameter is small and the true value lies well outside the confidence region. While it is easy to understand why the estimate is relatively poor (there is less data relevant to its estimation), but why is the confidence interval so narrow. This is an artefact of the bootstrap. In order to improve the fitting time, we start the parameters from their least-squares values. The non-linear optimiser will carry on moving parameters around as long as there is significant improvement in the objective function. If the parameter is having too small an effect, the parameter will not be moved (by default). Hence, a parameter may take on similar consecutive values because the likelihood surface with respect to the parameter is very flat. So, it has very little effect on the sum-of-squares even if it is moved some distance. Because the non-linear optimiser concentrates on the local behaviour of the parameter, it gives up moving it although it may be a long way from its maximum point. While this is not necessarily a problem in the sense that the maximum point is probably not much of a better estimate than the current point, it does suggest in simulations that the parameter is much more accurate than it really is. This problem needs to be guarded against. One option is to increase the precision of the optimiser. Unfortunately, this is will greatly slow up the fitting process and does not guarantee success. A second is to try different starting points either between simulated data sets or for the same data set. This is preferable, but the software managing the bootstrap will need to be more sophisticated as the fitting process is much more likely to hit problems requiring intervention.

**Table 10.15 Results from fitting the model to simulated data, including bootstrap average and 90% confidence interval from 500 simulations. Perusal of the table indicates that the model fit performed well overall, and that the stock is heavily overfished. As can be seen from the "true values", used to simulate the real data, this is the correct interpretation. Where there are biases, they are correctly identified by the bootstrap. This general result is no surprise as the structural errors are minimal (i.e. the model used to simulate the data was largely the same as that to fit the model).**

| Year 1994 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| True Values | 461026 | 103220 | 85468 | 16110 | 2655 | 5602 | 2900 | 1165 | 407 | 116 | |
| Least-Squares | 517903 | 106974 | 93494 | 16161 | 2831 | 5972 | 3044 | 1303 | 560 | 230 | |
| Average | 518083 | 105438 | 97466 | 17305 | 3027 | 6644 | 3311 | 1440 | 597 | 223 | |
| 0.05 | 516218 | 90626 | 84678 | 15456 | 2546 | 5746 | 2779 | 1199 | 489 | 181 | |
| 0.95 | 520313 | 118067 | 115511 | 19853 | 3604 | 7830 | 3888 | 1718 | 726 | 272 | |
| Age 10 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1984, 11 |
| True Values | 1618 | 2374 | 2810 | 4145 | 5496 | 4806 | 4301 | 1293 | 929 | 515 | 1507 |
| Least-Squares | 892 | 1137 | 1866 | 3491 | 6141 | 5654 | 4154 | 1645 | 1073 | 602 | 386 |
| Average | 650 | 971 | 1712 | 3136 | 6018 | 5734 | 4169 | 1795 | 1113 | 638 | 222 |
| 0.05 | 553 | 870 | 1559 | 2902 | 5737 | 5510 | 3981 | 1669 | 1051 | 585 | 172 |
| 0.95 | 765 | 1099 | 1903 | 3406 | 6299 | 5993 | 4344 | 1904 | 1177 | 687 | 288 |

| Reference Points | S1994 | S% | Bunexp | B1994 | B1995 |
|---|---|---|---|---|---|
| True Values | 0.158 | 0.099 | 1991735 | 48747 | 30059 |
| Least-Squares | 0.182 | 0.114 | 2079070 | 57994 | 31435 |
| Average | 0.183 | 0.115 | 2080709 | 63877 | 43365 |
| 0.05 | 0.172 | 0.108 | 2070741 | 55964 | 36179 |
| 0.95 | 0.194 | 0.122 | 2104842 | 75664 | 53947 |

The relatively poor estimate of these recruits affects the reference points, causing their confidence intervals to be too narrow. This makes little difference ultimately to the interpretation, however. The least-squares estimate for the projected 1995 spawning stock biomass ironically is closer to the true value despite the evident bias.

There were other errors introduced, most notably the proportional use of GPS and monofilament gears assumed by the analysis was not true in the simulated data. These and other sources of uncertainty should ideally be included in the simulations. These would widen the confidence intervals, which would then include the true values.

# 11 SPREADSHEETS WITH EXAMPLES AND EXERCISES

The Examples described in Chapter 10 and additional Exercises can be found on the Compact Disk that is provided with this manual. For further explanations please consult the file Software.doc.

The methods explained are for illustration only and should not be taken as an endorsement of any particular method or software. In some of the examples, data presented were extracted from ICES assessment working group reports. These data do not represent all information available for stock assessment, as they were selected to illustrate the methods only. The results differ from the ICES stock assessment results and should not be used for anything other than illustrating calculations.

It is hoped that the users will be given enough insight to evaluate methods for themselves and see whether any technique is applicable to their own data and fisheries. All software routines are written in Visual Basic for Applications and the exercises and examples are given in Microsoft Excel (Office 97 Service release 2, or later).

## EXCEL SPREADSHEETS OF EXAMPLES AND EXERCISES

| | |
|---|---|
| **Example 10**<br>**Example 10 Bootstrap** | These worksheets contain the example models, described in Chapter 10 of the manual, including Visual Basic for Applications routines. |
| **Acoustic Survey** | The ADAPT model uses an acoustic survey as the abundance index. The method is the same as that used for other indices, except that we can treat the survey as an absolute estimate, so the parameter adjusting the proportionality of the index, q, can be ignored. |
| **ADAPT with 1 index** | Make a spreadsheet to perform an ADAPT estimation of stock size and fishing mortalities for Baltic cod in Sub-Divisions 25 - 32 using Pope's cohort analysis. Use only 1 CPUE observation series as the abundance index. |
| **ADAPT with 2 indices** | Perform an ADAPT on North Sea Cod data with external weighting on 2 surveys. Use backward extension i.e. F(10) =average F(7-9). Use a given external weighting for the sum of squares of each series. |
| **Estimate $F_{med}$** | Make a spreadsheet to calculate $F_{med}$ for Baltic cod in Sub-Divisions 25 – 32. Use the Thompson and Bell procedure for calculating the SSB per recruit. |

| | |
|---|---|
| **Estimate $F_{msy}$ $F_{crash}$** | Estimate the reference point fishing mortalities for maximum yield ($F_{msy}$) and the point where the fishery becomes unsustainable ($F_{crash}$). |
| **Fit Stock_Recruit Model** | Fit Beverton and Holt, and Ricker models to the Baltic Cod Subdivisions 25-32 estimates of R(age2) and SSB. The data on Recruitment and SSB are the output of an ICA analysis of the data for Baltic Cod Subdivisions 25-32 |
| **ICA** | Carry out an Integrated Catch-at-age Analysis (ICA) for Baltic cod in Sub-Divisions 25 - 32 with one abundance index. Note that ICA uses a separable VPA model. |
| **ICA Missing Catch** | Make a spreadsheet program to perform an ICA for Baltic cod in Sub-Divisions 25 - 32 treating 1991 as having no observed catch. This can be done by splitting the model into a separable VPA 1991 onwards and a normal tuned VPA before 1991. The separable VPA uses an estimated exploitation rate to provide an estimate of the catch. |
| **PopeCohortAnalysis** | Make a spreadsheet to perform a VPA for Baltic cod in Sub-Divisions 25 - 32 using Pope's cohort analysis. |
| **Retrospective** | Make a spreadsheet to perform a retrospective analysis for Baltic cod in Sub-Divisions 25 - 32 using ADAPT framework. |
| **Sensitivity** | Make a spreadsheet to perform a VPA for Baltic cod in Sub-Divisions 25 – 32 using Pope's cohort analysis and carry out a sensitivity analysis on the results. |
| **SeparableVPA** | Make a spreadsheet to perform a Separable VPA for Baltic cod in Sub-Divisions 25 – 32. |
| **ShortTermProject** | Set up a spreadsheet to project stock status variables into the short term for Baltic Cod including TAC. The model should be ordinary VPA. |
| **StandardiseCPUE** | Set up a Log-linear model to standardise CPUE indices (Cpue RV surveys data for Baltic cod in 25 – 32 subdivisions 1990 –1996). The regression will require dummy x-variables. Use the Analysis Tools regression add-in. |

The spreadsheet models are complicated and not easy to follow in all cases. Flow diagrams have been given where appropriate. Another tool which is useful for tracing cell links is the Audit add-in provided with Excel. This will be worth using to see how cells are calculated.

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Virtual population analysis (VPA) is a widely used model for the analysis of fished populations. While there are many VPA techniques, they vary in the way they use data and fit the model rather than in the form of the model itself. This manual describes the common VPA model and the assumptions on which it is based, together with descriptions of associated diagnostic procedures and common reference points. More important, the manual describes the numerical techniques that can be used to fit the model based on weighted least-squares, which is the basis for the ADAPT approach. The techniques are described so that they are readily implemented in a spreadsheet. General methods and specific examples are given to enable readers to develop an approach suitable for their own data and fisheries

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